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May 7, 2004, 12:59:49; Search time 9150.23 Seconds (without alignments) 10942.062 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Sequence:

Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Total number of hits satisfying chosen parameters:

Searched:

2: gb\_htg:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CI2NIS/09, A01K67/033, CO7K14/705, CO7K16/28, CI2NI/21, CI2NIS/10,

CI2NI/68,

PC G01N33/15, G01N33/50/(CI2NI/21, C12R1:19), C12NIS/00.C12NIS
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/organism="Drosophila melanogaster"
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    Patent: JP 200023680-A 1 25-JAN-2000;
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ITFAIIIRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLN WVAETHVATSDAVPLWIRIVFLOWLPWIIRMSRPGRPJILDEFPTTPCSDTSSERCHQI LSDVELKERSSKSLLANVLDIDDFRHVPROTTPGGTLPHNPAFYRTVYGGGDGSIG PIGSTRANPATHTCIKSSTRYELGIILKEIRFITDQLRKDDECNDIANDWKFAAMV VDRLCLIIFTWFAILATIAVLLSAPHIIVS"	Query Match 100.0%; Score 2310; DB 6; Length 2886; Best Local Similarity 100.0%; Pred. No. 0; Matches 2310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	. Qy 1 ATGAAAATGCACAACTGAAACTGACTGAQTTGACGATGATGAGGTGGCTGGCAGTA 60	OY 61 AGATTAGCGCACTGCAGCAGCAGCAGCAGTAGCAGTAGCAGCACAGAACCACCAGCAGC 120	OY 121 AACCAGAGGACAACCAGGAACTCACAACACTGCAAGGAGCTTAAGTACAAACAC 180	OY 181 CACAGCAACATTGCAAGCGAGCAGCACAATAGCCAGCAACAGGAGCCAGCATCGAAGGAC 240	OY 241 GAGGATGTAGCCACCGGTAGAAGCAATGACCAGCAGAAGCAATCTGCAACAGCTAGAC 300	OY 301 AGCAGCAACAIGITGTCGCCAAAGACAGCAGCAGCAACTGCTGCCGGCGATGAAGCA 360	QY         361 ACAACCCAACAACCAAACATAAGACTGTGCACGCAAGCGACAACGATTGCGTCGC 420           Db         732 ACAACCCAACAACAAACAAACAAACAAGAATATCAAGAAACAACGACTTGCGTCGC 791           QY         421 GGACGAAAAAGAAAACCAGCAACCCCAAACGAATATCAAGAAACAACAACAACTT 480           Db         792 CGACGAAAAAGAAACCAGCAACCCCAAACGAAACAACAAAAAA	481 AGCATGCCTCCCTTCAAAACGCGCAAATCCACGGACACCTACAGCACCACCAGCAGCAACAACAACAACAACAAAACAAAAACGCAAAATCCACGGAACACTACAACAACCAAC	OY 541 ACCAGCIGACAGCCACATACAGAGAGGAGGAGGAGAGAATAGAGTAGAGTAT 600  Db 112 ACCAGCTGTCCGACACCTACATGCAATGCGACCAGCGACAATGAGTTCAGTATT 971  OV 601 CCGATATCGAGACAAGGAACCACCACCACACACACACACA	972 CCGATATCGAGACATGATAGAGTATCCACGGCCACATTCGCCTGGGTTTGCATGTCTTG	OY 661 CAGGIGCTGCTGCTGCAACAGTGGCAACTTCACGTGCAACAGCGATCGGTGCTA 720  1032 CAGGIGCTGCTCGTGTGCAACAGTGCCAACTTCACGTGCAACAGCGATCGGTGCTA 1091	Oy 721 CTGTTCAGAAGGATCGCAGCGAGCACCATCGCTTCATTTAGGCAGCTTTGCA 780	OY 781 GCGCAACTGAAAATAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAACAACA	OY 841 ACGCAAATATTAAACGGACTTAATAAACACTCATGGATATTTTATTGTTGTTTTGAAT 900  1212 ACGCAAATATTAAACGGACTTAATAAACACTCATGGATATTTTATTGATATTTGAAT 1271	QY 901 FIATCTGCTAAAGTTTGCCTAGCAGGATATCATGAAAAAGAGTTACTGCAGATCTTTTG 960
	Qy         1921 AACGTACTAGACATGATGACTTCCGGCACAATTGTCGCCCCATGACGCCCGGCGGA 1980	OY 1981 ACACTGCCACACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGC 2040  Db 2352 ACACTGCCACACACCCGGCTTTCTATCGCACGGTTTATGGACAAAGGCGACGATGGCAGC 2411	Qy 2041 ATTGGGCCAATTGGCAGCACCCGAATGCCGGTCACCCCATCATACGTGCATCAAA 2100	Qy 2101 TCATCAACTGAATATGAATTAAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAG 2160  Db 2472 TCATCAACTGAATATGAATTAAGGTTTAAAGGAAATTCGCTTTATAACTGATCAG 2531	Qy 2161 CTACGTAAAGATGACGAGTGCAATGACATTGCCAATGATTGGAAATTTGCAGCTATGGTC 2220	OY 2221 GTTGACAGACTGTGCCTTATCACAATGTTCGCAATATTAGCCACAATAGCTGTA 2280	QY         2281 CTACTATCGGCACCACATATTATTGTCTCG         2310           Db         2652 CTACTATCGGCACCACATATTATTGTCTCG         2601	RESULT 2 AX009610 LOCUS AX009610 BETINITION Sequence 1 from Patent EP0962528. VERSION AX009610 VERSION AX009610.1 GI:9996842	KEYWORDS SOURCE Drosophila melanogaster (fruit fly) ORGANISM Drosophila melanogaster ORGANISM Brosophila metanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Fohndroidas, Procombilidas, Procombilidas	REFERENCE 1 AUTHORS Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. TITLE Nucleia caids encoding acetylcholin-receptor subunits from insects JOHNAL PALENT: EP 0962528-A 1 08-DEC-1999	G G	/organism="Drosophila melanogaster" /mol type="unassigned DNA" /db_xref="taxon:7227" CDS 3722684	/note /codo /prot	7499" VDDDELWLAVRLAHCSSNFSSSSS KNSQQQEPASKDEDVANHGRSNDQ MTDT CANDAGE TABLERAND WITH TABLERAND WITH TABLERAND WITH THE TABLERAND	MINDS TATABATES THAT TOGETH TO THE TRANSMENT OF THE THAT THE TRANSMENT OF	DFLAGGERGATYOTHY TO WEALEWN DEMAKEN TO GGENTULK FFHK IWKPDYLMYNBADGGFDGTYOTHYVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRC EMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPBPYID

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Drosophila melanogaster (fruit fly)

Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Booptera; Endopterygota; Diosophila.

Boydroidea; Drosophilidae; Drosophila.

En (bases 1 to 2834)

S Grauso, M., Reman, R.A., Culetto, E. and Sattelle, D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalphas, Dalpha and Dalpha7, in Drosophila melanogaster Identify a

Now and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-Mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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SMPPFKTRKSTDTYSTPAAITGCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
VLQVLLVSLQQMQLHVQRSYLLFRSIAASTTAFISYLGSPAAQLRSSSSSSSNSNS
GNSSSTQILNGLNKHSWIFLIYULISAKVCLAGYHBKRLHDLLDPYNTLERPVLNE
SDPLQLSFGLTLMQIIDVDERQQLLVTNVWIKZLEWNDMNLEWNTSDYGGVKDLRIPP
RIWKPDYLMYNSADEGFDGTYQTNVVNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
CEMKFGSWTYDGFQVCPANVTRSITTAARNPI"
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NQQLTTLQPRSLSTKHHSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSS
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Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds, alternatively spliced.
AY036613
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/note="ion channel; neurotransmitter transmembrane
receptor; exon 5 is excluded due to exon skipping,
generates a loss of reading frame and a truncated
polypeptide; alternatively spliced"
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1 3QX, UK
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Direct Submissor 1 to 2834)
Submitted (26-MAY-2011) MRC-FGU Human Anatomy and Genetic University of Oxford, South Parks Road, Oxford OX1 3QX, Location/Qualifiers
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/db_xref="G1:20340269"
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/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
/map="34E4-34E5"
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                      CTCAACGGCGAGTGGGAACTACTGGGTGTGCCCGGCAAACGTAACGAGATCTATTACAAC
                                        CTCAACGGCGAGTGGGAACTACTGGGTGTGCCCGGCAACGTAACGTAACTATTACAAC
                                                                                          TGCTGCCCGGAACCCTATATAGACATCACCTTCGCCATCATCATCCGCCGACGAACACTG
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	9 GIGCI CAACGCGAGGIGGGAACTACTGGGGGGGGGGGGGGGGGGG	1558 CTGIACUATTCTTCAACCTGATCATACCTTGTACTGATTGCCTCCATGGCCTTGCTC 1617	1678 TCGCTGACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTG 1737 1893 TCGCTGACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTG 1737 1738 CCATTG	ACGATTITAATATTATGATGATGATGGAAATGCTGATACGCACGAAATGTCCGAATGG A ATACGCATGGAAATGCTGATATTGCGAATGGAAATGCGAAAGAAGAAGAAGAAA A AAAAAAAAAA		1867 CAGATACTCTCCGACGTTGAGCTGAAAGAGCGCTCGTCGAAATCGCTGGCCAACGTA 1926	1987 CCACACAACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGCATTGGG 2046	2373 CAATTGGCAGCACCCGAATGCCGGATGCGCTCATCATACGTCCATCAATCA	2167 AAAGATGACGAGTGCAATGCCAATGATGGAAATTTGCAGCTATGGTGGTCGTTGAC 2226
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Db 2553 AGACTGCCCTATACATATTCCCAATGTTCGCAATATTGCCCAATGTTCGCAATATTGTCCCG 2310  Db 2613 TCGGCACCACATATTATTGTCTCG 2310	Querry Match         33.6%; Score 776.2; DB 2; Length 42079;           Beet Local Similarity 89.0%; Pred. No. 2.6e-201;         Anatches 902; Conservative 0; Mismatches 13; Indels 98; Gaps 2;           Qy         1 ATGAADAARTGAACTGAAACTGACATGACGATGACGATGACGACGAGTA 60           Db         10132 ATGAAAAATGCACGACAACTCAAGAGTGACGATGATGACGACGAGGAGTA 10191           Qy         61 AGATTAGGGCACTGACGACAACTCAGCAGACACAAGAACCACACAGAACCACCAGCAGG 120           Db         10192 AGATTAGGGCACTGACGACAACTCACACACACACACACAC

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Meoptera; Endopterayota; Diptera; Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.

1. (bases 1 to 186803)
1. (bases 1 to 186803)
2. (bases 1 to 186803)
3. (cliniker.S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Bvans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An.H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doupl, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalex, M. Houck, J., Hoskins, R.A., Hostin, D., Howland, T.U., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Mark, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Saveri, J.S., Smith, H.O., Rubin, G.M. region 35x-35x
                                               14350 ATCATATITAACTAAATATATAGAAATTTAGAAAATAATTGCACCCTCAGCACTTGAATT 14291
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Drosophila melanogaster, chromosome 2L, region 35X-35X, BAC clone
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Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
                                                                                                                                                                                                                                                      14230 AATCCACGGACACCTACACCACCAGCAGCAATAACCAGCTGTCGGACAGCCACCTACA
                                                                                                                                              14290 TGGTCTTCTTACAATTGCAGAAACAACAACAACTTAGCATGCCTCCCTTCAAAACGCGCA
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Perriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
1begwan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeitfer,B.,
Phouamenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                        Berkeley, CA 94720.
This sequence was assembled using end sequences from a whole genome shotgum and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14830 ATGAAAATGCACAACTGAAACTGACTGAAGTTGACGATGATGAGGTGGGCTGGCAGTA 14771
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                                                                                                                                                                                                                                        Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GAGGATGTAGCCAACCACGGTAGAAGCAATGACCAGCAGCAACGCATGTGCAACAGGTAGAG 300
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
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Pred. No. 3.4e-201;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                     Berkeley, CA 94720
This sequences assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Fhouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
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                                                                                                                                Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAGCAACATGTTGTCGCCAAAAGACAGCCGCAGCAGCAACTGCTGCCGGCGATGAAGCA
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/clone lib="RPCT-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 186803;
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Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 776.2; DB 3;
Pred. No. 3.6e-201;
0; Mismatches 13;
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Drosophila miclandyster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Roptera; Endopterygita;

Biphydroidea; Drosophila.

Ephydroidea; Drosophila.

Sadams, M. D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Ananatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,

George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,

Ran, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor, G.L.,

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Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D.,

Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beaaley, E.M.,

Beeson, K.Y., Benos, P.V., Bernan, B.P., Bhandari, D., Bolshakov, S.,

Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davemport, L.B.,

Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I.,

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Gelbart, W.M., Glasser, K., Glodek, A., Gong, P., Gorger, C., Kernis, C., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J.,

Wei, M.H., Theywam, C., Jalai, M., Kalush, F., Karpen, G.H., Ke, Z.,

Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,

Li, J., Li, Z., Liang, Y., Liu, X., Liu, X., Mattei, B., Murphy, E.,

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Drosophila melanogaster chromosome
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AE003642 AE002690 AE014134
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AUTHORS
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ECVPDCSASSPDNCRNGFCRSPGVCECFAEFVRNEHGACIHTCPIACQHGRCYLNGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="CG33119"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FLYBASE:FBgn0028543"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6532,6591. .6882)
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13:31:36 PST 2002"
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12:47:27 PST 2002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBgn0027929"
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gene="BG:DS00180.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="CG33119"
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                                                                                                                                                                                                                                                                                                                                                                                                   product="CG31765-PA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="BG:DS00180.12"
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Musskern, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinett, K., Remington, K., Saunders, R.D., Scheeller, S., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wanssenbach, J., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodager, Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zhong, W., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.

The genome sequence of Drosophila melanogaster

N. Science 287 (5461), 2185-2195 (2000)
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Scaniker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Banzon, J. An. H. Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Diedson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Gargo, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Montoca, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Stong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M., Sequencing of Drosophila melanogaster genome

Lu Unpublished

S. (base 1 to 272521)
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Submitted (23-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Sep 16, 2002 this sequence version replaced gi:7298121.
Location/Qualifiers
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Submitted (O-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 272521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 272521)
Matthews, B.B., Bayraktaroglu, L.,
Campbell, K., Hradecky, M.A., Matthews, B.B., Kaminker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.B., Clamp, M.E., Drysdalle, R.A., Emmert, D., Frise, E., de
Grey, A.D.N.J., Harris, N.L., Kromiller, B., Marshall, B.,
Millburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E.,
Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Annotation of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (bases 1 to 272521)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA 5 (bases 1 to 272521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus tag="CG31765"
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12:45:45 PST 2002"
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JOURNAL
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VOTED RANGE CONTRIBUTION OF THE PROPERTY OF	686 AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTTCACAAGGATCGCAGCGAGCA 745	9 DROSADHO2 320754 bp DNA linear INV 21-MAR-2000 ION Drosophila melanogaster, chromosome 2L, region 34C4-36A7 (Adh region), section 2 of 10 of the complete sequence. ON AE003408 AC001595 L39628 L39633 L43488 L42039 L39621 L42040 L43450 L4042 L39627 AC001302 AC000577 L42043 L39632 L39630 AC000578 L39635 L42041 L39637 L39636 L39624 L39631 L39625 L39634 L39623	L4449 L39626 L39620 L38632 AC001660 L39751 L49183 L42072 L33753 L33757 L33754 L42076 L42076 L33754 L42076 L33754 L42076 L33754 L42076 L42077 L39758 L42079 L39751 L49185 L42075 L39765 L43622 L39761 L39762 L39762 L39765 L42073 L39762 L39760 L43451 L39754 L42076 L42075 L39765 L42074 L42070 L39759 AC001662 L43488 L46890 L46894 L46892 L46891 L44487 AC001664 AC001202 AC000610 AC001304 AC000609 AC000613 AC000613 AC000612 AC002515 L79864 L43472 L76998 L79865 L43473 L79866 L43474 L42044 AC000592 L76999 AC004326 L43472	AC000556 AC001301 AC000557 AC000558 AC000559 AC000561 AC000561 AC000561 AC000562 AC000563 AC000563 AC000564 AC002866 AC002865 AC002865 AC002865 AC002866 AC002866 AC002867 AC002868 L39682 AC002869 L34342 AC002869 L3682 AC000624 L3432 AC000566 L39683 AC000567 AC003871 AC000622 L77011 AC000625 AC001796 L81440 L81336 L81334 AC001797 AC000626 I TA7019 AC003408 L81335 AE003406 AC003408 L81335 AE003408 AC003408	2 of 10 Drosophila melanogaster (fruit fly) M Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		'AL Genetics 153 (1), 179-219 (1999)  INE 9403001  Chases 1 to 320754)  RE 10471707  Celnikeri,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,  Butenhoff,C., Champe,M., Chavaz,C., Chew,M., Ciesiolka,L.,  Boyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,  Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karras,K., Kearney,L.,  Kim.E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,	AL
WORVTPPAHRYOVUDETALE HINCTRAMAGGOCTRACTACHAGGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6 6 6 6 6 6 6	RESULT DROSADF LOCUS DEFINIT ACCESSI		VERSION KEYWORI	SEGMEN SOURCE ORGAI REFEREI	AUTH	JOURI MEDL: PUB REFEREI AUTH	TITE
	vQPVTPPAHRYQVLDBTALFINKTRSAMASGVCYKEVPTASLIKNSRDOFVV MSRIQVCCDGYERNPHIYRRCEPICADDCRNGICTAPNTCVCIPGHVRTAER PLGCGMGVCDBRNBCKRERSYSLEPETRYRYQCPGCRGGRGVAPNRCA PADGGSCBPVCDSCBNGKCTAPGHICNCHAGYLKLQGRCEPICSIPCKGNGCTG ASGFEWDRKSAECLPKCDLPCINGVCVGNNQCDCKTGYVRDEHQRNICQPH GYCSAPNFCIPRGFIKSGIKGNGVCVGNNQCDCKTGYVRDEHQRNICQPH GYCSAPNFCIPRGFIKSGIKGNGVCVGNNQCDCKTGYVRDEHQRNICQPH GYCSAPNFCIPRGFIKSGIKGNGVCVGNNQCDCKTGYVRDEHQRNICQPH GYCSAPNFCIPRGFIKSGIKGNGVCN / Jocue Laga-EG3115" / Jocue Laga-EG3115" / Mapp="34E5-34E5" / Jocue Laga-EG33115-N / Jocue Laga-EG33115-N / Jocue Laga-EG33115-N / Product="CG33115-NA"	Similarity 89.0%; Pred. No. 3.9e-201; Conservative 0; Mismatches 13; Indels 98; Gaps ATGAAAAATGCACAACTGAAGTTGACGATGATGAGGTGTGGCTGGC	AGATTAGCGCACTGCAGCAGCACTTTAGCAGCAGTAGCAGCACAAGAACCACCAGCAGCAGCAGCAGCAGCAGCA	181 CACAGCAACATTGCAAGCGAGCACAATAGCCAGCAACAGGAGCCAGCATCGAAGGACCAGAATGAAGAGCACATCGAAGGACCCAGCATCGAAGAGACCAGCATCGAAGAGACCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGAAGA	301 AGCAGCAACAATGTTGTCGCCAAAGACAGCCGCAGCAACTGCTGCCGGCGATGAAGCA 03705 AGCAGCAACTATGTTGTCGCCAAAGACAGCGAGCAGCAACCAAC	421 CGACGAAAAGAAAACCAGCAACCCCAAACGAAACAGATATCA	ATCATATTTAACTAAATATAGAAATTTAGAAAATAATTGCACCTCAGCACTTGAATTAGAAACAACGCAACTTAGCATGCCTCCCTTCAAAACGCGCA TGGTCTTCTTACAATTGCAGAAACAGCAACTTAGCATGCCTCCCTTCAAAACGCGC AATCCACGGACACCTACAACAGCAACTTAGCATGCCTCCGACACACAC	TGCAATGTCGAGCCAGCGACAATGAGTTCAGTATTCCGATATCGAGACATGATGAGGTATTTCGATATCGAGACATGATGAGGTATTTCCATATCGAGACATGATTGAGGTATTTCCGATATCGAGACATGAGTATTCGAATGAGTTTCAGATTTCCGATATCGAGACATGAGTATTCAGATTTCCGATGATGAGGTATTCAGATTTCCGATGATGAGTATTCGAATGATTTCGAATGATGATGATGATGATGATGATGATGATGATGATGAT

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gene="Sog"
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On or before Mar 22, 2000 this sequence version replaced gi:237899, gi:237899, gi:285578, gi:237899, gi:3097819, gi:3095519, gi:3097819, gi:3097819, gi:3097819, gi:3097819, gi:3097829, g
                                                                                                                                                                                                                                                                                                                                                                                                              The orientation of this sequence along the chromosome is left to right. This sequence was annotated by Sima Misra (sima@fruitIty.DerKeley.edu) on Dehalf of the Berkeley Drosophila Genome Center. Coding sequences are predicted based on computational analysis, using both gene and CDS prediction programs and matches to other sequences. These predictions and matches been evaluated by the annotators and may have been refined by hand. The annotators have also used their judgement about which matches to include in this record. The annotations on this sequence can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.fruitfly.org/publications/Adh.html
The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v
1.2.
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SSLNFCCDDAQLESLERAIFKRFDCRTFKHTRFQPQRPQINIDPGIRFBFSQRSDWQP
SPNGLIWSQVPEELRPYEISVNGKRQGVTKKKMKTSQAALAISKYKLFLIFFLELVKFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Pl library, partial Sau3A in pNS582tet14Ad10 and RPCI-98 (Roswell Park Cancer Institute Drosophila melanogaster BAC library, partial EcoRI in pBACe3.6)" complement(135. .1376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(135. .447,505. .1376))
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'strain="y; cn bw sp"
'db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          examined in more detail from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/ translationsperieducourses
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7603. .853mbol=Sos"
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ESTIRQFFEQLDPFNGLSDKQMSDYLYNESLRIEPRGCKTVPKFPRKWPHIPLKSPGI
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GAVPISPHVNVPMATNMEYRAVPPPLPPRRKERTESCADMAQKRQAPDAPTLPPRDGE
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/gene="Sos"
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/db_xref="G1:728791"
/db_xref="FLYBASB:FBan9999001"
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species:''HOMO SAPIENS"
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GKRNEIYYNCCPEPYIDITFAILIRRKTLXYFFNLIVPCVLIASMALLGFTLPPDSGG 4; 1032 298 DMES54210

Losophila melanogaster mRNA for nicotinic acetylcholine receptor 238 972 178 Direct Submission Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WC1E 6BT, UNITED KINGDOM TTAATGCAAATTATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGTTTA CTCATGCAGATTATCGATGTGGACGAAAGAATCAACTGCTTATAACGAATATTTGGCTC GTTTGCCTAGCAGGATATCATGAAAAGAGCTGTTACACGATCTTTTGGATCCTTATAAT 119 gerirérgegécrégaccecardagagegécracrecadececérrergacaacracaac ACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACT Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. subunit /gene="nAcRalpha-18C" /product="nicotinic acetylcholine receptor subunit Dalpha7" product="nicotinic acetylcholine receptor subunit 135; Length 1683; AJ554210.1 GI:29466436 nAcRalpha-18C gene, nicotinic acetylcholine receptor Indels melanogaster" 0; Mismatches 436; DB 3; Score 515.4; DB Pred, No. 7e-130; subunit Dalpha7 (nAcRalpha-18C gene) Drosophila melanogaster (fruit fly) 1. .1683 /organism="Drosophila /gene="nAcRalpha-18C" 132. .1651 /mol\_type="mRNA" /db\_xref="taxon:7227" 'gene="nAcRalpha-18C" 'gene="nAcRalpha-18C" Location/Qualifiers 'codon start=1 Query Match 22.3%; Best Local Similarity 62.5%; Matches 952; Conservative 1 (bases 1 to 1683) Millar, N.S.

QY         2104 TCAACTGAATAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAGCTA 2163           Db         1433 TCTGCGGAGTACGAACTGGCGTGATACTCAGGAGCTGCGTTGGAACAGGTC 1492           QY         2164 CGTAAAGATGACAGTGAATTGCCAATGATTGGAAATTTGCAGCTATCGTCGTT 2223           Db         1493 AAAAAGAGGACGAGATGAATTACGCCAATGGTGGAATTTGCTGCCATCGTCGTT 2223           QY         2224 GACAGACTGTGCCTTATTATTCATTTTCGCCAATATTGCTGCCATGGTGTTCT 2283           Db         1553 GATCGTTGCTTATTATTTCACCTTGTTTACTATTATAGCACATGGTGTTCT 1612           QY         2284 CTATCGGCCCATATTATTTCACCTTGTTTACTATTATAGCAACCTCGCTGTACTC 1612           Db         1513 TTCTCGGCGCATTTATTGT 2306           Db         1613 TTCTCAGCCCCATATTATTGT 1635	AF143846 N Heliothis v 7-1 subunit AF143846 AF143846.1 Heliothis v Heliothis v Eukaryota, Neoptera; E	REFERENCE 1 (bases 1 to 3629)  AUTHORS Schulte, T., Oellers, N. and Adamczewski, M.  TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits.  JOURNAL Unpublished  REFERENCE 2 (bases 1 to 3629)  AUTHORS Schulte, T., Oellers, N. and Adamczewski, M.  TITLE Direct Submission JOURNAL Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18,, Leverkusen 51368, Germany, FEATURES Location/Qualifiers	source  3629   /organism="Heliothis virescens"   /organism="Heliothis virescens"   /organism="Reliothis virescens"   /organism="Heliothis virescens"   /obxef="taxon:7102"   335. 1825   /obxef="taxon:7102"   /odon_start=1   /odon_start=1   /odon_start=1   /odon_start=1   /ototein_id="AAD32697.1"   /obxef="fa:4895005"   /obxef	VIILSLIVFLAMWAEIMPATSDAVPLIGTYFNCIMFWVASSWVSTILLINYHRHAD THENSUMBURCVETYRRGGEBRGAGLAHSCFGVDFELSLILKEIRVITDOMRKD DEDADISRDWRFPAMWVDRLCLIFFLIATLAVLLSAPHIMVS"  Query Match 22.2%; Score 512.8; Ded. No. 4.3e-129; Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;  Qy 925 GGATATCATGAAAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACGT 984  Db 425 GGGTACCACGAGAAGCGCTACTGATTTTGGACCACTATAATACACTAGAACGT 484
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1 (bases 1 to 3701)
Martin,A., Nadja,E. and Thomas, S.
Mucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 2 25-JAN-2000;
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                               CCGGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAG
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DIATIPVEKKREDVLAYNSADGFDFTHTNIVKHNGSCLYVPPGIFKSTCKIDITW
FPFDDQHCENKFGGATYDGNQLDJVLNSEDGGDLSDFTTNGWYLLAMGKKNTIVYA
CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSWALLGFTLPPDSGEKTTLGYTIL
BESTTVELNTARETLEQVSDALPLGFTFOLTERPWASSVYLTYVLINYHHRTADIHEM
PEWIKSCYFLOMLPWILLEMGREGKTTRKTTLLISNRKELELEKERSSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCHHKDLHLIKELQFITARMRKADD
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (1-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/mol_trpe="mRNA"
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/note="results in isoleucine
compared to variant clone"
/replace="g"
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/protein_id="AAM13392.1"
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/dev_stage="embryo"
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bobtera; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2023)

Grauso,M., Reeman,R.A., Culetto,E. and Sattelle,D.B.

Novel Putative Nicotinic Aectylcholine Receptor Subunit Genes,

Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify in New and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002)
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BLEITPRKLKREDVLAYTSABEGFOFTYTHNIVVKHGSGSCLYVPPGIFSTGTCKNDITW
PPEPDOGHCEKKEGSYTYDGNGLDLVINSEDGGDLSDFITNGFWYLLAMFGKKGYTIVYA
CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
ELSTYTVELNYABRTLEQVYBALPLGFTYFNCIMPWASSVYLTVVLIXHHRTADIHEM
PPWIKSYFLOALPWILDSRYFRTIFFYFNCIMPWASSVYLTVVLIXHHRTADIHEM
PPWIKSYFLOALPWILDSRYFRTIFFYFNCIMPWIELELKERSSKGLLANTDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELOFITARMRKADD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to serine substitution; compared in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein id="aam13394.1"
db_xref="GI:20152849"
'translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                  8b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
                                                                                                            OXI
                                                                                                                                                                                                                                                                                                                                                                                                            /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681 CAAGGATCTACGAATCACGCCCAACAAGCTGTGGAAGCCCGACGTGCTCATGTACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561 GACGCTGCAGCAGCATCATCGACGTGGACGAGAAGAATCAGCTTCTCATAACGAATCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 raaagaaagcrercaaggaccreaagaaaaggeeergeergeaaccarergergergeera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           969 TAATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTITAATGCAAATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GITAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGT
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                      Tobases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                organism="Drosophila melanogaster"
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Pred. No. 1.4e-109;
0; Mismatches 574;
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to the sequence deposited
AE003626"
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'gene="nAcRalpha-30D"
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                                                                                                                                                                                                                /mol_type="mRNA"
/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                              'gene="nAcRalpha-30D"
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                                                                                                                                                        Location/Qualifiers
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.. .2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variant type III"
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Best Local S:
Matches 824
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    PUBMED
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1580 2090 1640 2150 1700 2210 2270 1820

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1821 GGITACGGIGCTGCTGCGCTCCGCACATAATCGT 1856

Search completed: May 8, 2004, 02:41:13 Job time : 9171.23 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- nucleic search, using sw model OM nucleic

7, 2004, 10:08:00 ; Search time 929.055 Seconds (without alignments) 10562.710 Million cell updates/sec Мау Run on:

US-09-303-232-1 COPY 372 2681

1 atgaaaaatgcacaactgaa.......caccacatattattgtctcg 2310 Perfect score: Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

6747726

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

geneseqn2001as:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

Abl27131 Drosophil Abl27130 Drosophil Abl07799 Drosophil Aaz24476 H. viresc Drosophil Drosophil H. viresc Drosophil Human PRO Human neu Neuronal Human neu Human neu Mutant hu Mutant hu Wild-type Human neu Description Abl13733 I Abl07231 I Abl07231 I Abl07798 I Aac58395 I Aac90380 W Aav12197 I Abr48239 M Abs54875 I Abr3248 I Abr73248 I Abr73248 I Aac90386 N Aav44687 V Aac90387 N Aat59197 N Abz11298 H Aat59196 N Aac90385 SUMMARIES ABL27130 ABL07799 AAZ24476 ABL13733 ABL07231 AAZ24477 ABL07798 ABV73248 ADA10864 AAC90385 AAC90386 AAC58395 AAC90380 AAT48239 ABS54875 AAV44687 AAC90387 AAV12197 AAZ24475 DB Length 1540 3109 14668 1509 1509 1876 1876 1876 1876 1509 1509 1509 1509 2101 2101 2886 984 3700 1876 936 Query Match 1 2310 881 766.2 5310 612.3 4411.2 4411.2 296.2 296.2 296.2 296.2 296.2 296.2 296.2 296.2 294.6 Score Result

Human neu		Human neu		Neuronal	Prostate	Human neu	Himan 205	Human 205	Chimeric	DINA ANG		Himan nic								1 -	5
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AAV12199	AAQ90387	ABS54870	ABV73243	AAT48235	ABK92165	ADA10854	ADC71170	ADC71168	AAC90382	AAS91552	AAT59527	ADB78668	ADB78671	ADB78670	ADB78661	ADB78672	ADB78663	ADB78669	ADB78662	ADB78673	ADE85024
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## ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds D. melanogaster acetyl-choline receptor DNA from clone Da7. /\*tag= a /product= "acetyl choline receptor." AAZ24475 standard; cDNA to mRNA; 2886 BP Location/Qualifiers 372. .2684 (first entry) Drosophila melanogaster. 17-FEB-2000 AAZ24475; RESULT 1 Key AAZ24475 

DE19819829-A1.

11-NOV-11999

melano

98DE-01019829 04-MAY-1998;

98DE-01019829 04-MAY-1998;

(FARB ) BAYER

Schulte T; Adamczewski M, Oellers N,

WPI; 2000-014207/02. P-PSDB; AAY50814 New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim 1a; Page 8-12; 26pp; German.

V274T var Mutant hu

Human pol Neuronal

Neuronal

AAT59197 ABZ11298 AAT59196

283.8 267.8

284.4

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as

1200

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1380 1751 1440 1811 1500 1871 1560 1931 1620 1991 1680 2051

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AAGCACCAGATACTCTCCGACGTTGAGCTGAAAGAGCGCTTCGTCGAAATCGCTGGTGGCC
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                                                             GATCCTTATAATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGC
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                                                                                                                                                                               AATGTGTGGTTAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCCTCCGACTAT
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        insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
2352 ACACTGCCACACACCCGGCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB27377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863
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                                                                                                                                                                                                                                                                                                                                                                                                            AATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCAT 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATTTGACGGCACC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCAGACGAGACGTGGGGGGAACAACGGCTCGTGTCTATACGTTCCGCCGGGGATC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAGCGGTGCGAG 1353
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                                                                                                                                 is.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention isseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL01840-ABL16175) and the encoded proteins (ABB01815).

ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                          isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                              GACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGACATG
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                                                                                                                                                                                                                                                                                                                               : 99
                                                                               Claim 1; SEQ ID NO 17879; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                   Length 803;
                                                                                                                                                                                                                                                                  Sequence 803 BP; 211 A; 199 C; 190 G; 203 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              15; Indels
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88.4%; Pred. No. 1.8e-138;
iive 0; Mismatches 15;
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616; Conserv
 P-PSDB; ABB63696
                                                       interactions.
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              985 CCCGITCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTTAATGCAAATT 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurotransmission; plant protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3700;
                                                                                                                                                                                                                                                                                                                                                      virescens acetyl-choline receptor DNA from clone Hva7-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic; insect; insecticide;
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AAZ24476 standard; cDNA to mRNA; 3700 BP.
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les 878; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heliothis virescens.
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                                                                                                                          AAZ24476;
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                                                                                                                    AGACTIGLECTTATTATETTTACCCTGTTECACAATCATCGCCCACGCTAGCCGTGCTGCTG 1798
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175
                                                                              developmental biology; cell signalling; insecticide;
                   ВP
                  CDNA; 1540
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2000US-00614150.
                                                                                                                                                   23-MAR-2001; 2001WO-US009231
                                               (first entry)
                                                                                                     Drosophila melanogaster
                                                                                      gene;
                 standard;
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                                                                                      pharmaceutical;
                                                                                                                   WO200171042-A2
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                ABL07231
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                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL10176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                          ATTTTTCAATTTAATTGTGCCATGTGCTAATCTCATCGATGGCCCTACTGGGCTTCA
                                                                                            CCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGA
                                                                                                                                                                                 CCGIGITICIGAATAIGGIIGCCGAGACAAIGCCGGCTACTICCGAIGCGGIGCC 1739
                                                                                                                                                                                                           screening;
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neurotransmission; plant protection agent; conductance; AChR; ds
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Best Local Similarity 68.8
Matches 565; Conservative
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                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating call signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGTG-ABL30511), expressed DNA sequences (ABLG1040-ABL30515) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1053 GGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGGAACGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACCAGACGAACGTGCTGCTGCGGAACAACGGCTCGTGTCTATACGTTCCGCCGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          Sequence 14668 BP; 4616 A; 3078 C; 2662 G; 4312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 14668;
                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                    Claim 1; SEQ ID NO 17876; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1300 GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGGT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                     7.4e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Score 335.8;
Pred. No. 7.4
                                            Myers EW;
                                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC58395 standard; cDNA; 1509
                                                                                                                                                                                                                                                                                                                                                                                        14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                    99.48;
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                                           <u>:</u>:
                                                                                                                                                                                                                                                                                                                                                                                                                Matches 337; Conservative
                                                                                                              New isolated nucleic
                                           Adams M,
                                                                    2001-656860/75
              PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                   WPI; 2001-656860
P-PSDB; ABB63695
                                                                                                                                            interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2001
                                         Venter JC,
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             (PEKE)
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO294, PRO341, PRO355, PRO619, PRO717, PRO809, PRO8103, PRO1005, PRO1007, PRO1101, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1187, PRO10081, PRO 10081, PRO10081, 
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AACSB36 and AABS4057 to AACSB36 represent human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO Polynucleotide and protein sequences given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 ACGIGICCCIGCAAGGCGAGIICCAGAGGAAGCIIIACAAGGAGCIGGICAAGAACIACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes an isolated antibody that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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Pred. No. 2.9e-72;
0; Mismatches 318;
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99US-0141037P.
99US-0143048P.
99US-0145698P.
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al Similarity 60.7%;
506; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood WI;
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Best Local Similarity
Matches 506; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB24088
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                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-2000;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe CK,
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CCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGC 1390
                                                            Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                                                                  The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AxC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAACCTGATCATACCTTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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Pred. No. 2.9e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with none or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
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764 CIGCAGATICCGGGGAGAGATITCCCIGGGGAIAACAGICTIACTCTCTTACCGICI
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/product= "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                neuronal nicotinic acetylcholine receptor; alpha-7 subunit; tissue; screening; NAChR; antibody; ds.
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Best Local Similarity
Matches 506; Conserv
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide
AGCCCTACCCGATGTCACCTTCACAGTGACCATGCGCCGCAGGACGATCTACTATGGCC
                                                       TCAACCTGATCCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCTGC
                                                                                       TCAACCTGCTGATCCCCTGTGTGTCTCTCGCCCTCGCCCTGCTGGTGTTCCTGCTTC
                                                                                                                                   CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT
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                                                                                                                                                                                                            TICTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
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                                                                                                                                                                                                                                                                                                                                                                       of the
                                                                                                                                                                                                                                                                                                                                                                                             esb.
                                                                                                                                                                                                                                                                                                                                                                   A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of th human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for identifying cpds. that modulate the activity of human nAChRs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                         Nucleic acids encoding nicotinic acetyl:choline receptor sub-units in screening to determine the effect of drugs on the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 296.2; DB 2;
Pred. No. 3.3e-72;
); Mismatches 318;
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 71-73; 108pp; English.
                                                                                                                                        (SIBI-) SIBIA NEUROSCIENCES INC
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                                                                 96WO-US009775.
                                                                                                     95US-00484722.
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60.7%;
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nes 506; Conservative
                                                                                                                                                                            Harpold MM
                                                                                                                                                                                                                    WPI; 1997-065463/06.
P-PSDB; AAW09025.
                                                                 07-JUN-1996;
                                                                                                       07-JUN-1995;
                                                                                                                                                                              Elliott KJ,
                           27-DEC-1996
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immunochemistry; NAChR alpha7 subunit;

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Location/Qualifiers

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                                                                                                                                                     TAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTA
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                                                               AAGTITGCCTAGCAGGATATCATGAAAAGAGCTGTTACACGATCTTTTGGATCCTTATA
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                                     6
     Length 1876;
                                     Indels
                                    0; Mismatches 318;
     DB 6;
   12.8%; Score 296.2; DB (60.7%; Pred. No. 3.3e-72
                              506; Conservative
                 Similarity
Query Match
Best Local S:
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Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.

Elliott KJ;

Siegel R,

Chavez-Noriega LE,

29-OCT-2001; 2001WO-US0509B5 01-NOV-2000; 2000US-00703951

WO200259266-A2.

01-AUG-2002

(MERI ) MERCK & CO INC

Gillespie A,

2002-698532/75.

P-PSDB; ABB82435.

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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, substantially free of contamination from many other receptor proteins, substantially perform in vitro screening of the drug substance on a particular system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
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1090

304

1150

424

Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;

neuronal NAChR alpha7 subunit encoding cDNA

22-JAN-2003

MX BX BX BX BX B

Human

standard; cDNA; 1876 BP

ABV73248 ABV73248

RESULT 15 ABV73248

425 CIGAIGAGGGITIGACGCCACAIICCACACIAACGIGIGAAIICTICIGGGCAII 484	1271 GTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCC 1330	485 GCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATGATACGTGTACGTTTC 544	1331 CCTICGAIGACCAGCGGIGCGAGAAGITCGGCAGITGGACCTACGACGGAITCCAGC 1390	545 CCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGGAGGTGGTCCT 604	1391 TGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG 1450	605 TGGATCTGCAGATGCAGGAGGCAGATATCAGTGGCTATATCCCCAATGGAG 655	1451 AGTGGGGAACTACTGGGTGTGCCGGCAAACGTAAGGGGATCTATTACAACTGCTGCCCGG 1510	656 AATGGGACCTAGTGGGAATCCCCGGCAAGAGGGTGAAAGGTTCTATGAGTGCTGCAAAG 715	1511 AACCCTATATAGACATCACCTTGGCCATCATCATCAGCGACGACGACGTGTACTATTCT 1570	716 AGCCCTACCCCGATGTCACCTTCACAGTGACGCCGCGGGAGACGCTCTACTATGGCC 775	1571 TCAACCTGATCATACCTTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGC 1630	776 TCAACCTGCTGTTTCTCTCTCTCTCTCTCTCTCTTCTTGTTTCTTGCTTTC 835	1631 CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT 1690	836 CTGCAGATTCCGGGGGAGATTTCCCTGGGGATAACAGTCTTACTCTCTCT	1691 TTCTGAATATGCGGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743	896 TCATGCTCGTGGCTGAGATCATGCCCGCACATCCGATTCGGTACCATTG 948
Ob	ζ	QQ	δλ	DP .	δλ	q <sub>Q</sub>	ζŏ	qa	δλ	qq	δλ	qa	ò	qq	QY	QC

Search completed: May 7, 2004, 15:01:30 Job time: 939.055 secs

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7, 2004, 14:08:32; Search time 6207.93 Seconds (without alignments) 1111.850 Million cell updates/sec
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2310
1 atgaaaaatgcacaactgaa......caccacatattattgtctcg 2310
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BG632919 GH16126.3 AL058211 Drosophil AL073676 Drosophil AL064281 Drosophil
* Query Match Length DB ID	BG632919 CNS0001F CNS00HJU CNS006F9
DB	12 29 29
Length	885 1101 1007 978
* Query Score Match Length DB ID	18.4 14.4 14.3 14.0
sult No. Score	424.8 332.2 331.2 323.8
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589	3901 9013	5857	AK034228 Mus mu	3157 Mus	5337 UI-N	102873 Homo	02874	702422 UI-N	06232 Mus	29177 Mus mu	2344 UI-M-HB	19460 K-EST020	02875 Mus	497	51730 Mus	30415 Mus	31254 Mus	19722 Mus mus	1742	9954	AGEN	7186	5733	0475	5843	1715	7184	14206	3 / BUL	230	1000	K033068	11327 HOMO	4155 UI-M-GV0	89825 UI-M	3069 647	Y406231 Pan	760 B£lo:	02876 Homo
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## ALIGNMENTS

RESULT 1 BG632919/c LOCUS BG632919 885 bp mRNA linear EST 23-APR-2001	DEFINITION GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128 FBan0004128 (10n channel' located on: 21, 30n - 30F1: 04/10/2001 menh common	z	Σ			AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.			Contact: Stapleton, M. BDGP	Lawrence Berkeley National Lab	One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798	Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu	Based inon the presence of a VBoT site followed by a second of a	Σ	BG632919  GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster read pOT2 Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919  BG632919.1 GI:13758409  BG732919.1 GI:13758409  BC732000hila melanogaster (fruit fly)  Drosophila melanogaster (fruit fly)  Drosophila melanogaster (fruit fly)  Brosophila melanogaster (fruit fly)  Drosophila melanogaster (fruit fly)  Brosophila melanogaster (fruit fly)  Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., BDCP/HMI Drosophila EST Project  Unpublished (2001)  Cohner ESTS: GH16126.5prime  Contact: Stapleton, M.  BDGP  Lawrence Berkeley National Lab  One Cyclotron Rd, Berkeley, CA 94720, USA  Fax: 510 486 6798  Bmall http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGGT 451
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AL058211
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Matches 334; Conserv
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CNS0001F
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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003511: arm:X [18792641,19136447] estimated-cyto:1883-1866: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
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                                                                                                                                                                                                               /sex="male and female"
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/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Cygan: head; Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2. Plasmid cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                        Score 424.8; DB 12; Length Pred. No. 1.8e-92; 0; Mismatches 182; Indels
                                                                                                                           1. .885
/organism="Drosophila melanogaster"
/mol_trpe="mRNA"
/db_xref="taxon:7227"
/clone="GH16126"
                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.4%;
Best Local Similarity 74.6%;
Matches 534; Conservative
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Direct Submission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage : Branct Submission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Edopteray, Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR02C08"
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Pred. No. 8.2e-70;
1; Mismatches 4;
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us-09-303-232-1\_copy\_372\_2681.rst

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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkelsy Drosophila denome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at herry//haraation from the BACPAC Resource Center can be
                                                                                                                              CNS006F9 978 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR13X21 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 8.9e-68;
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/note="end : TET3"
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                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR35F05 of RPCI-98 library from Drosophila melanogaster (fruit AL073676
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/db xref="taxon:7227"
/clone="taxon:727"
/clone lib="RPCI-98"
/note="end : TET3"
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Best Local Similarity 98.2%;
Matches 333; Conservative
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AI292581
GHIS518.5Parime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GHI5518 5 similar to CG4128: FBan0004128 ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mENA sequence. AI292581
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1 (bases 1 to 607)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BORP/HHMI Drosophila EST Project
470 ACAGTGCTGATGAGGGCTTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTG
                                                                  GCTCGTGTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGT
                                                                                                                                GGCATTGCCAGTWCCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGCT
                                                                                                                                                                                               GGTTCCCCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003626: arm:2L [9617316,9882551]
estimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
High quality sequence stop: 521
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Other ESTs: GH15518.3prime
Contact: Stapleton, M.
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AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
Was incrmalized. Library was constructed by Life Technologies, a
division of Invitogen. This sequence belongs to sequence cluster
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03QP1&cluster=7646.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12793792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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          GATGAAGTTCGGCAGTTGGACCTACGACGATTCCAGGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP05"
                                                                                                                                                                                                                                                                                                                                                    AL530299.2 GI:31068132
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                                        /dev stage="adult"
/lab_host="DHS - alpha"
/clone lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head, Vector: pOT2; Site 1: EcoR1; Site 2:
XhoI: Sized fractionated cDNAs were directly ligated into
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                         TAAAGAAAGCTGTCAAGGACCTCAAAAAGCGCCTGCTGAACCATCTGCTGTCCACCTA
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90134548 Single gene library Homo sapiens CDNA, mRNA sequence.
CD013901
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                                                                                                                                                        Score 265; DB 9; Length 60
Pred. No. 1.7e-53;
0; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jin, P., Fu, G.K., Wilson, A.D., Yang, J.,
Au-Young, J. and Stuve, L.L.
PCR isolation and cloning of novel spli
                             sex="male and female"
 xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug target genes
Unpublished (2003)
Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
db_xref="taxon:7
clone="GH15518"
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                                                                                                                                                       11.5%;
Similarity 71.4%;
19; Conservative
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                                                                                                                                                                                                   /clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was perfor using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 251; DB 14;
Pred. No. 7.2e-50;
0; Mismatches 330;
                                                                                                                                   sapiens"
                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                             Email: pjin@incyte.com.
Location/Qualifiers
                                                                                                                                organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%;
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                                                                                                                                                                             CCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGACATCACC 1530
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337 AACCTGAAGTTTGGCTCTTGGACCTATGGTGGTCACTTGACCTGCAGATGCTGAGA 396
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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                                                                      1411 GAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTGGGTGTG
                                                                                                                             397 TCA-----GACATATCTGAATATATCGTAAATGGAGAGTGGGACCTTGTAGGCGTT
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Functional annotation of a full-length mouse CDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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/lab_host="DH10B (phage-resistant)"
/clone_llb="NICHD_XGC_OO1"
/clone_llb="Vector: pcWv-SPORT6; Site_1: Not1; Site_2: Sal1;
Cloned_unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Kenopodinae; Xenopous.

1. (Dases 1 to 922)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGI-CGAP clone distribution information (clund through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI4228 row, Column: 14
High quality sequence stop: 746.
                                                                                                                                                                                                            Xenopus laevis cDNA clone
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Pred. No. 3.8e-46;
0; Mismatches 268; Indels
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/organism="Xenopus laevis"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                     922 bp
AGENCOURT 10492745 NICHD XGC_OO1
IMAGE:6642638 5', mRNA sequence.
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/db_xref="taxon:8355"
/clone="IMAGE:6642638"
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                  1713 AATGCCGGCTACTTC 1727
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S. Adachi, U. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizune, W., Hayashida, K., Hayatu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kati, H., Kaya, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kojima, Y., Mayazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Myazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, Y., Saito, R., Saitoh, H., Sakai, K., Shibata, Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-722 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLCISVLLSLTVFLLLITEI PSTSLVI PLIGEYLLFTMI PVTLSI VITVFVLNVHH
RSPRTHTMPAMVRRVPLDI VPRLLFMKRPSVVKDNCRRLIESMHKMANA PRFWPEPES
RPGILGDI CNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 (b11)-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2940)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tränslation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEERLLK
RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTTNVWVKOEWHDYKLRW
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                                   FANTOM Consortium and the RIKEN Genome Exploration Research
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//note="unnamed protein product; cholinergic recepnicothin; a laba polypeptide 4 (MGD|MGI:8788, GB|NW_015730, evidence: BLASIN, 99%, match=1946)
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Fax:81-45-503-9216)
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/db_xref="MG1:3398424"
/db_xref="taxon:10090"
/clone="9330165116"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="GI:26329799"
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/strain="C57BL/6J"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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polypeptide 4, full insert sequence.
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Gaps

3;

Score 232.6; DB 11; Length Pred. No. 2.4e-45; 0; Mismatches 344; Indels

10.1%; 56.6%;

Query Match 10.1 Best Local Similarity 56.6 Matches 452; Conservative

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RLESCYNKWSREVANISDVULVREGISIAQLIDVDEKUQMTTNVWKQEWHDYKLEN
DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLITKAHLFYDGRVQMTPAJYK
SSCSIDVTFRPPDQQNCTMKFGSWTYDXAKIDLVSWHSRVDQDFWBSGEWILVDAVG
TYNTRXYECCAEIYPDITAPIIRLDFLFTINLIIESCLITLISCHTULVFYLESGEWILVDAVG
TYNTRXYECCAEIYPLIITAPIIRLDFLFTINLIIESCHTULJFTITVTESTVITVFVLNYHH
RSPRTHTMPAWVRRVFLDIVPRLITAFIIRRPSYVKDNCRELIESMHKMANAPERWEBEE
SCHOFINGGLSPAPTCNRMDTAVETQPTCRSPSHKYSPLANAPERWEBEE
SCHPPNSSGAPVLIKARSLSVQHVSSQGAAEGSIRCRSBIQYCVSQDGAASITESK
PTGSPASLYRRRQQUASQOTSPCKCTCKEBEPVSPITVLKAGGTKAPPQHLDFLSPAL
TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLEMMFIIVCLLGTVGLLEPPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                /protein id="BAC38788.1"
/db_xref="GI:26350297"
/translation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEERLLK
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                                                                                /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Direct Submission
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Submission
Administration (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Nuwazaki, A., Murata, Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, Y., Salto, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagama, A., Tarawa, A., Shibata, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3230)
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                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Fax:81-45-503-9216)
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/clone="IMAGE:683671"
/tissue_type="whole brain"
/dev stage="mbry or 13.5,14.5,16.5,17.5dpc"
/db_host="mbry or 13.5,14.5,16.5,17.5dpc"
/dab_host="mbry or 13.5,14.5,16.5,17.5dpc"
/dab_host="mbry or 13.5,14.5,16.5,17.5dpc"
/dlob_host="mbry or 13.5,14.5,16.5,17.5dpc"
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/dlob_host="mbry or 13.5,14.5,16.5,17.5dpc"
/dlob_then the library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6.791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence late not pite in the polyA tail
is ACGGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                         GIGIACIGALIGOCICCAIGGCCTIGCICGGAITCACCCIGCCGCCAGAITCGGGIGAAA 1648
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CDNA clone
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                                                                                                                                                             861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-'demail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
thtup://magg.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                     921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
742 CCTACGCCTTCATCATCCGCCGACTGCTCTTCTACACCATCAACCTTATCATCCCGT
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                                                                                                                                                                                                                                                                    1 (bases 1 to 833)
NIH-MC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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UI-M-FYO-cds-b-06-0-UI.rl NIH_BMAP_FYO Mus musculus IMAGE:6813671 5', mRNA sequence.
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/mol_type="mRNA"
/strain="C57BL/6"
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Length 833;

9.9%; Score 228.8; DB 14; 57.5%; Pred. No. 1.4e-44;

Query Match Best Local Similarity

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1101
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1 (bases I to 1436)

Clark, AG., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                    Gaps
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Mismatches
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                                                                                                                                                                                                                                                             אומ 1436 bp DNA linear GSS 15-DEC-2003
Pan troglodytes CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. 1 (Dases 1 to 1436)
11 (Dases 1 to 1436)
12 (Add, M.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reriaira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
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677 GCTCATCTCCTTCCTCACTGTGCTCGTCTTCTACCTGCCCTCCGACTGCGGTGAGAAGGT
                                           1653 ATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCGAGAC
                                                                                 737 gacccidideairircigiceiereereereaceargiireeerggaaraacidagae
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/mol_type="genomic DNA"
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/gene="CHRNA3"
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                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitseion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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.larity 56.1%; Pred. No. 1.1e-43;
Conservative 0; Mismatches 346; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                          CTACCAGACGAACGTGGTGCGGAACAACGGCTCGTGTCTATACGTTCCGCCGGGGAT 1292
                                                                                                                                                                                                          CTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCAGCGGTGCGA 1352
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UI-M-FI0-byx-p-12-0-UI.rl NIH_BMAP_FI0 Mus musculus cDNA clone
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Email: cgapbs-r@mail.nih.gov
Irsue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 75.0)
NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/mol\_type="mRNA" /strain="C57BL/6"

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1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCACGAC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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                  /tissue_type="whole brain"
/dev_stage="embryo12.5dpc"
/lab_nost="bH10B (TI phage resistant)"
/clone lib="NH1B BNAP F10"
/note="Organ: Brain; Vector: pXx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agargee
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Pred. No. 2.3e-42;
0; Mismatches 299;
clone="IMAGE:6400763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%;
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Best Local Similarity 57.74
Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTGGTTAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGC 1143
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                                                                                                                                                                                                                                                             GSS 15-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1374)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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                                                                                                                                                                                                                                                        AY406232 13-DEC.
Mus musculus CHRNA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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GGCGAGAAGGICACGCIGIGCAICICGGIGCIGCIIITCICICACCGICIICCIG 748
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Pred. No. 3.5e-42;
0; Mismatches 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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/db_xref="taxon:10090"
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/locus_tag="HCM2488"
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Mus musculus (house mouse)
Mus musculus
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ORGANISM
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REFERENCE
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Job time : 6225.93 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:09:28 ; Search time 66.2366 Seconds (without alignments) 3284.615 Million cell updates/sec May on:

Run

US-09-303-232-2

1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 4043 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

geneseqp1980s: \*
geneseqp2000s: \*
geneseqp2001s: \*
geneseqp201s: \*
geneseqp201s: \*
geneseqp203s: \*
geneseqp203bs: \* A Geneseq 29Jan04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Aav50814 D. melano	. H	Ξ	Dro		_	Ade57308 Rat Prote	Rat	Neur				Aab82690 Nicotinic	Aab50012 Wild-type					Ade57310 Human Pro	Aaw69216 V274T var	Aabs0015 Mutant hu	6 Mutant	Mutant	2 Drosoph	
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de	Query Match	100.0	45.8	39.8	37.1	34.8	29.5	29.0	29.0	28.9	28.7	28.7	28.7	28.7	28.7	28.7	28.7	8	28.7	28.7	α	28.5	28.4	28.3	27.8	24.5
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Aael2824 Caenorhab	Abp96318 Caenorhab	Aab50014 Chimeric	Aab50018 Mature ce	Aaw44155 Human neu	Aar73966 Alpha 2 s	Aaw09021 Neuronal	Abq61850 Prostate	Abq31800 Human neu		Ada10855 Human neu	Human	Human	Add45584 Human Pro	Ade59169 Human Pro	Ade59167 Rat Prote	Add45583 Rat Prote	Abb59012 Drosophil	Ade57314 Human Pro	Ade57318 Human Pro
AAE12824	ABP96318	AAB50014	AAB50018	AAW44155	AAR73966	AAW09021	ABG61850	ABG31800	ABB82430	ADA10855	ADC71171	ADC71169	ADD45584	ADE59169	ADE59167	ADD45583	ABB59012	ADE57314	ADE57318
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. D. melanogaster acetyl-choline receptor protein from clone Da7. AAY50814 standard; protein; 770 AA. 17-FEB-2000 (first entry) Drosophila melanogaster AAY50814; RESULT 1

AAY50814

AAY50811

AAY50814

AAY508

DE19819829-A1.

11-NOV-11999

98DE-01019829. 04-MAY-1998; 98DE-01019829 04-MAY-1998;

(FARB ) BAYER AG.

Schulte T; Adamczewski M, Oellers N,

2000-014207/02. WPI; 2000-014207/ N-PSDB; AAZ24475. New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example la; Page 12-14; 26pp; German.

acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) datso vectors containing it, its regulatory regions, and antibodies distored against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetylcholine receptor isolated from Drosophila melanogaster This invention describes a novel nucleic acid (NA) encoding a nicotinic

Sequence 770 AA;

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                           Gaps
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere which can be used as an (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 NQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                    New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMALLGFILPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.8%; Score 1850; DB 3; 70.0%; Pred. No. 7.2e-161; ive 30; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS
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                                                                                                                                                                                                                                                                   Example la; Page 17-19; 26pp; German.
                                                                                                                                                Schulte
                                                       98DE-01019829
                                                                                       98DE-01019829
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Best Local Similarity 70.03
Matches 361; Conservative
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                                                                                                                                                                                             N-PSDB; AAZ24476.
                                                                                                                    P.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 496 AA;
                                                                                                                                                Adamczewski M,
                                                                                                                    (FARB ) BAYER
                                                         04-MAY-1998;
                                                                                       04-MAY-1998;
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SMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVA 305
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                                                 SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                              -WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                      SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                                                               673 YGQG-----DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 37938; 21pp + Sequence Listing, English.
                                                                                                                                                                                                                           DECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 37938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1498.5; DB 4
Pred. No. 8.3e-129;
4; Mismatches 3;
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97.4%;
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Best Local Similarity 97.4
Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
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N-PSDB; ABL14485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                     Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                         virescens acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.8%; Score 1609; DB 3; 60.8%; Pred. No. 1.1e-138; iive 57; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example la; Page 22-23; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                               Schulte
                                                  AAY50816 standard; protein; 501 AA.
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                                                                                                                                                                                                                Heliothis virescens.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ24477
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                                                                                                                                                                                                                                                                                                                                                                                             Adamczewski M,
                                                                                                                                                                                                                                            DE19819829-A1.
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                                                                              AAY50816;
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Sequence 311 AA;
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                                              Matches 257;
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                        Query Match
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                                              HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA 120
                                                                      HSN11ASEÓHNSOOGEPASKDEDVANHGRSNDOOTHLOOLDSSNMLSPKTAAAATAAGDEA 120
                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention iseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABR3072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                             181 TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQMQLHVQQRSVL
                                                                                                                                                                                            LFRRIAASTIAFISYLGSFAAQLKNSSSSS-SSNSSNNSSTQILNGLNKHSWIFLLIYL
               MKNAQLKLTEVDDDELWLAVRLAHCSSNISSSSSTRTTSSNKRHNQQLTTLQPRSLSTKH
                                                                                                TIQQPINIRLCARKRQRLRRRRRRRRRPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT
                                                                                                                                             TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 17841; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 17841
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                                                                                                                                                                                                                                                                                                                               ABB63683 standard; protein; 311 AA.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
interactions.
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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N-PSDB; ABL07786.
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                                                                                                                                                                                                                                            NLSAK 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in
                                                                                                                                                                                                                           79 DEKNQLLITNIWLKLEWNDMNLRWNSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                                                         139 YATNVVVRNNGSCLYVPPGIFKSTCKIDITWPPFDDQRCEMKFGSWTYDGFQLDLQLQDE
                                                                                                                                                                                                                                                                                                                                                                                                                               199 AGGDISSFIINGEWDLLGVPGKRNEIYYNCCPEPYIDITFAILIRRKTLYYFFNLIVPCV
                                                                                                295 LLIY----LNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                DEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                  YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDE
                                                                                                                                                                                                                                                                                                                                                                                                  TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCV
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuronal alpha-bungarotoxin binding protein alphal subunit.
                                                 Indels
34.8%; Score 1407.5; DB 488.6%; Pred. No. 1.8e-120;
                                                 18; Mismatches
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW12368 standard; protein; 502
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                                                    Conservative
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                          Similarity
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Costigan M;

Befort K,

'n

D'urso

Woolf C,

2003-268312/26

GENBANK; Q05941.

26-NOV-2001; 2001US-033347P.

HOSPITAL

(GEHO ) GEN HC (FARB ) BAYER

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recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal and albha2 subunits can also be used to produce subunit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location
                                                                                                                                                                                        295 LLIYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV 351
                                                                                                                                                                                                                                                                     TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALLIRRRTLYYFFNLIIPCV 531
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                                                                                                                                                                                                                                                     DEKNQLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 IVGLSVVVIVIVLQYHHHDPDGGKMPKMTRVILLNWCAWFLRMKRPG-----EDKVRPAC 357
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                                                                                                                                                                                                                                                                                                                              --ADISGYISNGEWDLVGIPGKRIESFYECCKEPYPDIIFIVIMRRRILYYGLNLLIPCV
                                                                                                                                                                                                             ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCS
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
                                                                                                                                                                  75;
                                                                                                                                  29.2%; Score 1179.5; DB 2; Length 502; 45.7%; Pred. No. 3.7e-99; tive 80; Mismatches 127; Indels 75;
                                                                                                                                                                 127; Indels
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                                                                                                                                                al Similarity
237; Conserv
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                                                                                                       Sequence 502 AA;
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The invention in European a composition comprissing two or more isolated rac derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a composition of that increases or decreases the expression of the polymuclectide sequence that increases or decreases the expression of the polymuclectide sequence that is differentially expressed in neuronal tissue of a first animal composition of a polymuclectide sequence which regulates the expression of a polymuclectide sequence which regulates the expression of a polymuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a polymuclectide sequence which is differentially expressed in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polymuclectide or the compound that complete its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of injury (CCI) and spared nerve injury (SNI)) in an animal constriction the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed construction in the configuration which is differentially expressed during pain in the configuration in the configurati
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                                                                                                                                                                                                                                                                                                                                                 invention discloses a composition comprising two or more isolated rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLI
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                                                                                                                                                                                                                                                                                                   Claim 1; Page; 1017pp; English.
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the polypeptide given the polypeptide given in the polypeptide given in the polypeptide given in the polypeptide given the polypeptide given in the polypeptide given procession of the pol
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                                               -----PPTSNGNLLY--IGFRGL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                 CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV
                                                                                                 ---GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDE
                                                                                                                                                                                                                                SEVICSEWKFAACVVDPLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                                                                                                                        CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein AAC33136, SEQ ID NO 12737
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                                                    -----LASVELSAGAG-
                                                                                                                                                                                                                                                                                                                                                                                   ADD47049 standard; protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-268312/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus.
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                                                                                                      673 YGQ--
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                                                                                                                                                                                                                                                                                                                                                                                   304
                                                                                                                                                                             67
therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                       245 SALALLVFILPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                                                                                                                                                                                                                                                                                                                                                                            305 GLSVVVTVIVLRYHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGEDKVRPACQHKPRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                       354 KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                         TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                         GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                        185 ADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTYTVTMRRRTLYYGLNLLIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                               -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PPTSNGNLLY--IGFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGQ-----GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDE
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                             534 ASMALLGFILPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding protein alpha 2; cholinergic;
                                                                                                                               85;
                                                                                                      Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal alpha-bungarotoxin binding protein alpha2 subunit.
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEVICSEWKFAACVVDPLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                      ; Score 1173.5; DB 7;
; Pred. No. 1.3e-98;
80; Mismatches 119;
                                                                                                      29.0%; Score 1173.5; 45.6%; Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31. .511
/label= Mat_protein
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LASVELSAGAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW12369 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuronal alpha-bungarotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligand binding; ion channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                Matches 238; Conservative
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  -----
                                                                               Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1997
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                                                                                                        Query Match
                                                                                                                       Local
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AAW44153
               The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neutronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal as immunogens for preparing antibodies to produce subunit peptides for use subtypes and their histological location
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 NGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 QPSNGNMIYSYHTMENPCCPQNNDLGSKSGKITCPLSED--NEHVQKKALMDTIPVIVKI 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLCLWASLFLSFF-----KVSQQGESQRRLYRDLLRNYNRLERPVMNDSQPIVVELQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WIRIVFLCWLPWILRMSRPG---RPL
                                                                                                                                                          New isolated neuronal alpha-bungaro-toxin-binding protein DNA - us screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        117;
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                                                                                                                                                                                                                                                                                                                                                                                                                           28.9%; Score 1168; DB 2; 44.2%; Pred. No. 4.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      83; Mismatches
                                                               INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                    Example; Fig 3A-B; 18pp; English
           89US-00413947
                                   89US-00413947
                                                                                          Schoepfer RD;
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                                                                                                                     WPI; 1997-118297/11
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 238; Conserv
                                                                                                                                  N-PSDB; AAT59197
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 511 AA;
                                                                                           Lindstrom JM,
           28-SEP-1989;
                                                                (SALK ) SALK
                                     28-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit ombinations with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtypes.
than drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     should lead to the identification and design of compounds that are expable of very specific interaction with one or more receptor subtracts that resulting drugs should exhibit fewer unwanted side effects that identified e.g. screening with cells that express a variety of subt
                                                                                                                                                                                                                                    Human, neuronal nicotinic acetylcholine receptor, alpha-7 subunit,
brain tissue, screening, NAChR, antibody.
                                                                                                                                                                         Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= cytoplasmic loop
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
AAW44153 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 80-81; 99pp; English.
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label= signal
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/label= TMD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= TMD2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= TMD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-303024/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9420617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elliott KJ,
                                                                                                                  14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1994
                                                          AAW44153;
                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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Score 1159.5; DB 2; Length 502; Pred. No. 2.6e-97;

28.7%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding nicotinic acetyl:choline receptor sub-units - used in screening to determine the effect of drugs on the receptor.
                                                                                                                                                                                                                                   304
                                             67
                                                                                  TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
                                    SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                                                                                                                                                                                                                         305 GLSVVVTVIVLOYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACOHKORR
                                                                                                                                                                                                                                                                                                                                                    669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                     IYLNLSAK - - - VCLAGYHEKRLIHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                     KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                 TWVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                               GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                            534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                           -WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                        CSDTSSERKHQ1LSDVELKERSSKSLLANVLD1DDDFRH----NCRPMTPGGTLPHNPAF
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 91;
                                                                                                                                                                                                                                                                                                                              CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP-
                                                                                                                                                                                                                                                                                                                                                                                                                 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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 Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 502
 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US009775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
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237;
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The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAcNR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48299). Host cells, esp. mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunit, see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
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                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                            297 IYLNLSAK---VCLACYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                        KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                                                                                                                                             TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCBMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIPCVLI
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                                                                                                                                                                                                                                91;
                                                                                                                                                                                               Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP
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                                                                                                                                                                                           28.7%; Score 1159.5; DB 2; 45.1%; Pred. No. 2.6e-97; ive 82; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO2145 protein sequence SEQ ID NO:77.
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                                                                                                                                                                                                              Similarity
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO6195, PRO10105, PRO10184, PRO1117, PRO1111, PRO1151, PRO1181, PRO2145 OR PRO1281, PRO213, PRO1197, PRO1111, PRO1151, PRO1182, PRO1184, PRO1187, PRO1181, PRO1184, PRO11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNQLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
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                                                                                                                                                                                                                                                                                                                                                   Roy MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91;
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                                                                                                                                                                                                                                                                                                                                                 Hillan KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.7%; Score 1159.5; DB 45.1%; Pred. No. 2.6e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis and prevention of cancer
                                                                                                                                                                                                                                                                                                                                               Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 61; Fig 58; 286pp; English.
                                                                                                                                     99WO-US012252.
99US-0141037P.
99US-0143048P.
99US-0145698P.
99WO-US028313.
                                                                              2000WO-US000376
                                                                                                                                                                                                                                           99WO-US030911
                                                                                                                                                                                                                                                                  2000WO-US000219
                                                                                                                                                                                                                                                                                                                                               Baker KP,
Wood WI;
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                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
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N-PSDB; AAC58395.
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WO200053755-A2
                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ,
Watanabe CK,
                                                                                                                                                                                                                                                                  05-JAN-2000;
                                                                              06-JAN-2000;
                                                                                                                                                                                  07-JUL-1999;
                                                                                                                                                                                                   26-JUL-1999;
                                                                                                                    08-MAR-1999
                                                                                                                                         02-JUN-1999
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                                                                                                                                                                                                -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
              SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues Tyr210,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues Trp171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                            CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                    669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                  305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGGDKVRP-ACQHKQRR
                                                                                                                                       CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP
534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                           OBSSEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                           724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171. .173
/note= "conserved ligand-binding region,
and Tyr173 are essential"
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/note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210. - 217
/note= "conserved ligand-binding region,
Cys212, Cys213 and Tyr217 are essential"
                                                       WIRIVFLCWLPWILRMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Tyr115 are essential"
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                                                                                                                                                                                                                                                                                                                                                                                                               Nicotinic acetylcholine receptor alpha7.
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2000EP-00203810
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31-OCT-2000;
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Human, alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.

WO200073431-A2. Homo sapiens.

gated ion channel.

Wild-type human alpha7 ligand

(first entry)

14-MAR-2001

conserved throughout the various nach a sequence includes regions that are essential for ligand binding. The invention relates to water-soluble seasontial for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AChBBPs) and analogues of ligand-gated ion channels, the mater-soluble ligand-binding proteins are capable of coming multimers and are amenable to crystallization. The crystal commendation of a comming multimers and are amenable to crystallization. The crystal special proteins are capable of coming multimers and are amenable to crystallization. The crystal complete in provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AChBP capable of binding a ligand of a ligand-determining solubility of the AChBP, in the same positions as in the determining solubility of the AChBP, in the same positions as in the chimeric proteins, at least the amino acids of at least of the conserved regions of an nAChR have been substituted for the corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that selectivally intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is fourette's syndrome, and prefered disorder is fourette's syndrome, and sequely and addiction to nicotine or schizophrenia 

502 AA;

Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.

Berkenpas MB;

Wolfe ML,

Groppi VE,

WPI; 2001-061524/07. N-PSDB; AAC90380

(PHAA ) PHARMACIA & UPJOHN CO.

99US-0136174P. 2000WO-US011862.

25-MAY-2000; 27-MAY-1999;

07-DEC-2000.

12; 353 473 184 533 244 581 612 668 401 413 304 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723 -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449 67 TWYLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 297 IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMQIIDVDE TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI -WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP 305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLINWCAWFLRMKRPGEDKVRP-ACQHKQRR CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGILPHNPAF KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------Gaps 91; ; Score 1159.5; DB 4; Length 502; ; Pred. No. 2.6e-97; 82; Mismatches 115; Indels 91; CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 28.7%; 45.1%; Matches 237; Conservative Local Similarity æ 89 128 474 185 364 450 414 245 699 724 Query Match 582 613 402

The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chineric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells ---HTCIKSSTEYELGLILKEIRFITDQLRK 723 305 GLSVVVTVIVLQYHHHDPDGGKMPKMTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 8 VWLALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTVYFSLSLLQIMDVDE TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---245 SALALLVFLLPADSGEKISLGITVLLSLTVFWLLVAEIMPATSDSVPLIAQYFASTMIIV KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI --WIRIVELCWLPWILRMSRPG----RPLILEFPTTP Gaps 91; DB 4; Length 502; 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP-534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-Indels / Match 28.7%; Score 1159.5; DB 4; Local Similarity 45.1%; Pred. No. 2.6e-97; les 237; Conservative 82; Mismatches 115; Disclosure; Page 61-63; 77pp; English 669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-Sequence 502 AA; 354 89 414 128 474 582 613 Query Match Matches q g d ð a ò 셤 à d ð à à à

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AAB50012 standard; protein; 502 AA AAB50012; RESULT 14 AABSO012 ID AABS XX AC AABS

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 IYLNISAK---VCLAGYHEKRLLHDLLDPYNTLERPYLNESDPLQLSFGLTLMQIIDVDE 353
---DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NACHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an; neuronal nicotinic acetylcholine receptor; nNAChR; receptor; flux; alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neuronal nicotinic acetylcholine receptor alpha 7 subunit
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                                                                                      Score 1159.5; DB 5; Length
Pred. No. 2.6e-97;
2; Mismatches 115; Indels
                                                       DDECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII
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92US-00938154.
93US-00028031.
93US-00149503.
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30-NOV-1992;
08-MAR-1993;
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                                                                                                                     SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
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                                                            ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIPCVLI
                                             GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE-
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                                   OM protein - nucleic search, using frame_plus_p2n model
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                                         /organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"
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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: BP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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ore: 4014.50 rcent Similarity: 95.42% ery Match: 3 3.00-203-203-201.700	US-U9-3U3-2312-Z (1-770) x AF272778 (1-2907)  QY	Oy 21 ArgLeuAlaHisCysSerSerAsnPheSerSerSerThrArgThrThrSerSer 40  349 AGATTAGCGCACTGCAGCAGCAACAACTTTAGCAGCAGCAGCAGAACCACCAGCAGC 40	Oy	Qy         61 HisSerAsnIleAlaSerGuGluGluHisAsnSerCalnGlnGlnGluDroAlaSerLysAsp		Oy 101 SerSerAsnMetLeuSerProLysThrAlaAlaAlaThrAlaAlaGlyAspGluAla	Qy         121 ThrThrGlnGlnProThrAsnileArgLeuCysAlaArgLysArgGlnArgLeuArgArg         14		Qy         161 SerMetProProPheLysThrArgLysSerThrAspThrTyrSerThrProAlaalaThr         180	Oy 181 ThrSerCysProThrAlaThrTyrMetGlnCysArgAlaSerAspAsnGluPheSer11e 200	Qy 201 ProlleSerArgHisAspArgValSerThrAlaThrPheAlaTrpValLeuHisValLeu 220	Oy 221 GlnValLeuLeuValSerLeuGlnGlnTrpGlnLeuHisValGlnGlnArgSerValLeu 240	ine;  Qy 241 LeuPheArgArglleAlaAlaSerThrIleAlaPheIleSerTyrLeuGlySerPheAla 260	Oy 261 AlaGinLeuLysAsnSerSerSerSerSerSerSerAsnSerSerAsnSerSerSer 	Oy 281 ThrGlnIleLeuAsnGlyLeuAsnLysHisSerTrpIlePheLeuLeulleTyrLeuAsn 300	Oy 301 LeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArgLeuLeuHisAspLeuLeu
Location/Qualifiers  12907 /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /chromosome="2t, 34E4-5"	/dev_stage="embryo" 1 2907 /gene="nAcRalpha-34E" /allele="A"	2892712	/product="nicotinic acetylcholine receptor Dalpha subunit" /protein id="AAM13390.1"	/WXFEE="G11:2015.2840" frainsi at ton="MKNAQLKIEVDDDELWLAVRLAHCSSNFSSSSSTRTT NQLITILQPRSLSTKHHSNIASEQHNSQQCEPASKDEDVANHGRSNDQOTHI. NNLISPKTRAAARTAGDERTTQQPTNIRLCARKRQRLRRRRKRKPATPNETDI	SMEPFKIRKSTDTYSTPARTTSCPTATYWQCRASDNBFSIFPISHDRYSTATFAWVLH VLQVILVSLQQDLHVQQRYVLLFRITAASTIJSTISTIGSFAAQLKNSSSSSSNSS NNSSTQILNGLNXGLNYGFRIFLLIYLNISAKVCLAGYHRKRLHDLLDPYNTLERPVINES DPLCLSFGLILNQTIDVDERNQLLVYNVMLKLENNDMLRWNTSDYGGVKDLRIPPHR THYRDDIV MANNA NOR OF THE	LWAEDVLARTNAADEGEDGIYQTINVVKNIGSCLIYVPPGEFKSTCKIDITWRPFDDDRC ENKEGSWYYDGFQLDJODETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYID ITPAIIIRRTLYYERVLIPCVLIAGMALLGFTLPPDSGEKLSGTJILLSTYVEN WAETWPATSDAVPLLGTYFNCIMFWVASSVVSTILILNYHRNADTHEMSEWIRIVF	LCWLPWILKMSRPGRPLILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDI DDDFRHNCRPMTFGGTLPHNPAFYRTVYGGDDGSIGPIGSTRMPDAVTHHTCIKSST EYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVUDRLCLIFTMFAILATIAVL LSAPHIIVS"	3/3 /gene="nAcRalpha-34E" /note="compared to B allele" /replace="a"	//gene="nAcRalpha-34E" /note="results in phenylalanine to isoleucine substitution; compared to B allele"	Ipha-34E" ts in threonine to isoleucine substi	cha-34E"	/recompared to B allele" /replace="gg" /replace="gg" /replace="gg" //replace="gg" //replace="gg"	ckd.pna->4£" sults in deletion of asparagine and ser to B allele" ""	<pre>LILY 1120 LILY 1120 /gene="mAcRalpha-34E" /note="results in serine, glycine, and asparagine /note="results in serine of parties" /ren]arcanasan</pre>	Jocaco ha-34E" jin asparagine to serine substitut	compareu to b allele" /replace="g"
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                                     AGCACGCAAATATTAAACGGACTTAATAAACACTCATGGATATTTTTATTGATATATTG
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Dalpha7"
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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26. .1674CRalpha-18C"
26. .1674CRalpha-18C"
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/product="nicotinic acetylcholine receptor subunit
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	726 GluCysAsnAspIleAlaAsnAspIrpLysPheAlaAlaMetValValAspArgLeuCys 745	QY
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US-09-303-2	706 GluLeuGlyLeuIleLeuLysGluIleArgPhelleThrAspGlnLeuArgLysAspAsp 725	δλ
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	615 AspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLys 631	07
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TO NEW STREET	5	δλ
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KEYWORDS	Alallellellelardronkvinsminster	ò
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AF143846 3629 bp mRNA linear INV 27-WAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha AF143846 GI:4895004

LOCUS DEFINITION

AF143846

ACCESSION VERSION

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Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hesinoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Heliothinae; Heliothis.
1 (Bases 1 to 3629)
Schulte, T., Oelleers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cezi
than to other insect nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MGGRARRSHLAAPAGLLLLCLLMPRGARCGYHEKRLLHHLLDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative nicotinic acetylcholine receptor alpha 7-1 subunit"
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Mismatches:
Indels:
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Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
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/organism="Heliothis virescens"
Heliothis virescens (tobacco budworm)
Heliothis virescens
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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 3 08-DEC-1999;
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                 LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPheAlaIle
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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1. .3700
/organism="Heliothis virescens"
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Heliothis virescens
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675 GlnGlyAspAspGlySerIleGlyProIleGlySerThrArgMetProAspAlaValThr 694  iii	AF321446 Drosophila melanogaster nicotinic acetylof subunit variant type II (nAcRalpha-30D) mi alternatively spliced. AF321446 AF321446.1 GI:20152846 Drosophila melanogaster (fruit fly)	Deptera; Endoperyota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  I (bases 1 to 2023) Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Gene Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Ide Naw and Highly Conserved Target of Adenosine Deaminase Actin RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002)	11973307 2 (base: Grauso,M Direct Si Submitte Genetics 3QX, UK	source 12023  / J. godinsm="Drosophila melanogaster"  /mol type="mRNA" /db rref="texon:7227"  /chromosome="2" /map="30D1" /dev stage="embryo"	/gen /gen /gen /gen /pro /pro /pro /pro /pro /pro /pro /pro
8 \text{8 \text{9 \text{8 \text{8 \text{9 \text{8 \text{8 \text{9 \text{	RESULT 9 AF321446 LOCUS DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS TITLE JOURNAL	O d	
	GlySetTrpThrTyAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGluThrGlyGly	515   Ilahrgargargtrangtrangtrangtrangtrangtrangtr		TCCTCCGTCGTCTCCACCATACTGATCCTCAACTTrp11eArg11eValPheLeuC	

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GluThrGlyGlyAspIleSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyVal 490
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'gene="nAcRalpha-30D"
'note="results in serine deletion; compared to variant
'note="results in serine deletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 MetAsnLeuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProPro
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                                                         to serine substitution;
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/note="compared to variant clone"
/replace="t"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                       'note="compared to variant clone"
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/note="results in asparagine
compared to variant clone"
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CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVELNIVABETLPQV8DA.PELGTYFNCINFWASSVYLTVVLLNYHHRTADIHEM
PPWITSVFLQWLPWILMREPGRYTITKTILLSNNKKELELKERSSKSLLANVLDIDD
DFRHTISGSQTALGSSAFRPTVEEHHTATGCNHVOLHLILKELQFITARNRKADD
BAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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                                                                                                                                                                               2023 bp mRNA linear INV 29-APR-2002 inicotinic acetylcholine receptor Dalpha6 (nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a and 8b"
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (Dases 1 to 2023)
Grauso, M., Reenan, R. Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify and Mighly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grauso, M. and Sattelle, D.B.
Direct Submission
Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="results in asparagine to glycine substitution;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2023
Coganism="Drosophila melanogaster"
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db_xref="taxon:7227"
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db_xref="G1:20152845"
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/dev_stage="embryo"
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auso, M. and Sattelle, D.B.
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subunit variant type I (
alternatively spliced.
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AF321445
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VERSION
KEYWORDS
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AUTHORS
TITLE
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370

642 390 702 410 762

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582

462 330 522 450 882 470

DEFINITION Drosophila melanogaster mRNA for nicotinic acetylcholine receptor accession AJ54209 about to balpha6 (nAckalpha-30D gene).  ACCESSION AJ54209.1 GI:29466434  KEYWORDS nAckalpha-30D gene; nicotinic acetylcholine receptor subunit Dalpha6.  SOURCE Drosophila melanogaster (fruit fly)  ORGANISM Drosophila melanogaster (fruit fly)  Rikarvora: Melanogaster arthronda: usanoda: receptor historia.	MANATORIA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  REFERENCE   (bases 1 to 1665) AUTHORS Millar,N.S.  TILLE Direct Submission JOURNAL Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, KINGDOM KINGDOM	HH///H/4	/gene="nAcRalpha-30D" /codon start=1 /product="nicotinic acetylcholine receptor subunit Dalpha6" /protein_id="CAD86935.1" /protein_id="CAD86935.1" /tanslation="MDSPLPASIFFULIFLAIIKESCQGPHEKRLINHLLSTYNTL /translation="MDSPLPASISIFVULIFLAIIKESCQGPHEKRLINHLLSTYNTL ERPVANRSEPLEVKFGILOOIIDVDERNOLLITNIMLGIEWNDYNIRWRFFFYGGYW	DLRITPNKLMKPDVLMYNSADEGFDGTYHTSVVVKHGGSCLYVPPGIFKSTCKMDITM FPRDOØHCBMKFGSWTYDGNQLDLVLSSEDGGDLSPITNGEWYLLAMPGKKNTIVYA CCPEPYUDIFTIQIRRILYYFPNLIVPCVLISSMALLGFTLPPDSGEKUTILGYTIL LSLTVELNLAAESMPTYSDAVDLGTYFNUINWASSVULTVVVVLNYHHRITADIHEW PPWIKSVFLQNLRBMPTSBAVDTSTRYTNILLSNRMKELELKERSSKSLLANVLDIDD DFRAITSGSQTALGSSASFGRFTTRKTILLSNRMKELELKERSSKSLLANVLDIDD EABLIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"  sig_peptide 44121	/gene="nAcRalpha-30D"  1221525 /gene="nAcalpha-30D" /product="nicotinic acetylcholine receptor subunit Dalpha6"	Alignment Scores: 3.89e-109 Length: 1665 Scores: 3.20 Horder: 320 Scores: 3.20 Conservative: 47 Best Local Similarity: 61.42* Mismatches: 75 Query Match: 3 Gaps: 79 DB: US-09-303-232-2 (1-770) x DME554209 (1-1665)	Qy         291 SerTrp11ePheLeuLeu11eTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyr         310	
Db   943 GAAGAIGGAGGATCTTCCGATTTCATAACAAIGGCGAGIGGTACTTGCTTGCCAIG   1002	531 ValleulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLyS		QY         582	Oy 614 SerAspThrSerSerGluArgLy8HisGlnIleLeuSerAspValGlu 629		DD 1573TCTGGCTCCCAAACCGCCATTGGCTCGGCCÄGTTCGGTCGG 1617  QY 690 ProAspAlaValThrHisHisThrCysIleLysSerSerThrGluTyrGluLbeuGly 708	Oy 729 AspileAlaAsnAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIle 748 ::::: 1735 GAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTGTTTAATTGTT 1794 OY 749 PheThrMetPheAlaIleLeuAlaThrIleAlaValLeuLeuSerAlabrOHisIleIle 768	OY 769 Val 769

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a high-throughput process to Collection 1 (Rubin et al., subjected to integrity checks polyA tail and contiguity believe the sequence to Max clone: However, there are ino of cDNA clones that may analyses such as internal segment. DNA, retained introns inced precursor RNAs, and sult in single base changes. Such including its location please visit our Web site.
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GCTGCAATCACAAGATCTTCAT 1339
                                                                                                                                                      alaspargLeuCysLeullelle 748
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TGGATAGATTTTGTTTAATTGTT 1459
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TGCGCAAAGCTGACGACGAAGCG 1399
erSerThrGluTyrGluLeuGly 708
                                                                          euArglysAspAspGluCysAsn 728
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lycera; Muscomorpha;
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One Cyclotron Road,
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Drosophila melanogaster (fruit fly)
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LLAMPGKKNTIVYACCPEPYUJITFIQIRRRTLYYFFNLJVPCVLISSMALLGGTLP
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YNYYHHRTADJHEMPPWIKSVFLQWLPWITNGRAFRYTTLLGNRWKELELKER
SSKSLLANVLDIDDDFRHTTSGSQTALGSSASFGRRPTTVEEHTTLLGNRWKELELKER
ELQFITARNRKADDEAELIGDWKFAAMVUDRFCLIVFTLIATVTVLLSAPHIIVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                    HisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProVal 330
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Matches:
Conservative:
Mismatches:
Indels:
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ORF"
                          product = "GH15518p
           codon_start=2
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λõ	531 ValLeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLys 550
qq	788 GIGCTAATCTCATGATGGCCCTACTGGGCTTCACATTGCCGCCGGATTCGGGCGAGAAA 847
oy B	551 LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu 570
8 8	71
qu	98 TCCATGCCGACAACGTCGGATGCTGTTCCTCTTATAGGCACCTACTTCAATTGCATCATG 96
δλ	581 581
qq	968 TTCATGGTCGCCTCGTCGGTGCTGACAGTAGTGGTGCTCAACTACCACCATCGCACA 1027
δγ	erencysTrpleuProTr
Db . 1	 Tacaatggctgccc
	4 IleLeuArgMetSerArgProGl
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ΟY	614 SerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGlu 629
Db 1	121ACACGCAAAACAATACTATTAAGCAATCGCATGAAGGAGCTGGAG 1165
٥y	erSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPh
Db 1	_ <u>5</u>
VO	650 ArgHisAsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyr 669
Db 1	226 CGGCACACAATA 1237
δλ	670 ArgThrValTyrGlyGlnGlyAspAspGlySerlleGlyProlleGlySerThrArgMet 689
Db 1:	238TCTGGCTCCCAAACCGCCATTGGCTCGCCAGCTTCGGTCGG
δλ	sSerSerThr
Db 1:	283 CCCACAACGGTGGAGGAGCATCACAGGGCCATCGGCTGCAATCACAAGATCTTCAT 1339
	709 LeulleLeulysGlulleArgPhelleThrAspGlnLeuArglysAspAspGluCysAsn 728
Db 1.	
~	729 AspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIle 748
Db 1.	400 GAATIGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGAATTTTGTTTAATTGTT 1459
	OHisileIl
Db 14	CACGCT
ŏ	769 Val 769
Db 15	520 GTG 1522
RESULT 13 AF321447	
DEFINITION	Ar521**, Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 Subunit variant type III (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
ACCESSION VERSION KEYWORDS	AF321447 AF321447.1 GI:20152848
SOURCE	Drosophila melanogaster (fruit flv)

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BRPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKMDITW
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CCPEPYVDITFTIQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWVASSVVLTVVVLNYHRTADIHEM
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DFRHTISGSQTAIGSSASFGRPTVEEHHTAIGCNHKDLHLIILKELQFITARWRKADD
EAELIGDWKPAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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GenBank Accession Number
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                                                                        Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b and
                                                                                                                                                                                  Chases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford C
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebyydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
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product="nicotinic acetylcholine receptor
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/mol_type="mRNA"
/db_xref="taxon:7227"
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to the sequence deposited
AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         id="AAM13394.1"
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/db_xref="G1:20152849"
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}79. .1863
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/dev_stage="embryo"
1. .2023
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variant type III'
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TITLE
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                                                                                                                                                                MetAsnLeuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProPro
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HisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrleuGluArgProVal
                                               LeuasnGluseraspProLeuGlnLeuserPheGlyLeuThrLeuMetGlnIleileAsp
                                                                                                         ValAspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAsp
                                                                                                                                                                                                                                   643 TACAATCTGCGCTGGAATGAAACGGAATACGGCGGGGCCAAGGATCTACGAATCACGCCC
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/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
                                                                                                                                                                                    /protein id="AmM13396.1"
/db_xref="G1:20152853"
/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
                                                                                                                               /product="nicotinic acetylcholine receptor Dalpha6 subunit
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/note="results in methionine to isoleucine substitution
compared to the sequence deposited in GenBank Accession
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Accession Number AE003626"
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Accession Number AE003626"
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/note="compared to the
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                                     CTAAAGGAGCGCTCCTCCAAATCCCTGCTGGCCAATGTCCTCGACGACGACGACGACTTC 1560
                                                                                                                                                                                                                                                                                                                                                                                                        CCCACAACGGTGGAGGAGCATCACACGCCCATC---GGCTGCAATCACAAAGATCTTCAT 1674
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Novel Putarive Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalphar, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAATTCTCAAAGAATTGCAATTTATTACGGCGCGGGATGCGCAAAGCTGACGACGAAGCG
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Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 2110)
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/db_xref="taxon:7227"
/chromosome="2"
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379. .1950
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1. .2110
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Grauso, M. and Sattelle, D.B.
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Necptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Cellian to other insect nicotinic acetylcholine receptor than to other insect nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                                                                     AF143847 100 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha AF143847 AF143847
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product="putative nicotinic acetylcholine receptor alpha
7-2 subunit"
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                                                                                                         700 LysSerSerThrGluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheIleThrAsp
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Schulte, T., Oellers, N. and Adamczewski, M. Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, 51368, Germany
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Matches:
Conservative:
Mismatches:
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Gaps:

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    /organism="Heliothis virescens"

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                                                                823 ATCTTCAAGAGCACATGCAAGATGGACATCACGTGGTTCCCATTTGATGACCAACATTGC
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                  LeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArg 314
                                                      LeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProValLeuAsnGluSer 334
                                                                                         AspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIleAspValAspGluLys 354
                                                                                                     AsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAspMetAsnLeuArg 374
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TGGAACGACGAGTATGGCGGGTCAAGGACCTCAGGATCACGCCCAACAAGTTGTGG 409
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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
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                                                                                                            This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter contained to ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II) This sequence encodes an acetyl-choline
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                                      New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
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                                                GlyArgProLeulleLeuGluPheProThrThrProCysSerAspThrSerSerGluArg
                                                           LysHisGlnIleLeuSerAspValGluLeuLysGluArgSerSerLysSerLeuLeuAla
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                LeuTrplleArgileValPheLeuCysTrpLeuProTrplleLeuArgMetSerArgPro
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on; plant protection agent; conductance; AChR; ds.
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotranamission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that aller conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
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                                                  nucleic acid encoding a nicotinic acetylcholine receptor cts, used to identify potential insecticides.
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Pred. No.:
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACCAGACC 469
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      nicotinic; insect; insecticide; screening; protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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          Acetyl-choline receptor;
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                                                     Heliothis virescens.
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Query Match:
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                                                                                                                                                                                                                              Adamczewski M,
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OY 415 ASNValValValValArgAsnAsnGlySerCysLeuTyrValProProGIVIlePheLysser 434	

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SASNASDIleAlaASNASpTrpLySPheAlaAlaMetValvalAspArgLew 744
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ing 1000 or more genes from Drosophila. The invention is
mental biology and in elucidating cell signalling and
tions in higher eukaryotes for the development of
rapeutics and pharmaceutical drugs. The invention
DWA sequences (ABL16176-ABB30511), expressed DNA
40-ABL16175) and the encoded proteins (ABB57737-
quence data for this patent did not form part of the
tion, but was obtained in electronic format directly
wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is acid detection reagent for detecting 1000 or more inla and for elucidating cell signaling and cell-cell
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2000US-00614150
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pharmaceutical; gene; ss.
                    Drosophila melanogaster.
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P-PSDB; ABB63128.
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                                      WO200171042-A2
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11-JUL-2000;
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                                    AGATTAGCGCACTGCAGCAGCAACATCAGCAGCAGTAGCAGCACAAGAACCACCAGCAGC
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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488 ATCTTCANAGACCACCACCACCACCACCACCACCACCACCACCACCAC	487 DB 1402 450 QY 717 547 Db 1459	137 aAlaMetValValAspArg	509 509	529 787 549	847 569 907	581 966	1026 . 581	1086	1146 XX 602 CC 1206 CC 62 CC 62 CC	1224 638 1284	r 658 Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Alia1 DB:	18Th 697
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681
                                                                developmental biology; cell signalling; insecticide;
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                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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New isolated nucleic acid genes from Drosophila and interactions.
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                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL04840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the princed specification, but was obtained in electronic format directly
detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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2 cDNA clones (AAM129196 and AAM59197) respectively code for the alphal subunit (AAM12368) and alpha2 subunit (AAM12369) of chick neuronal alphabungarctoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based on the N-terminal amino acid sequence of chicken brain ABBP. The probe isolated partial clone pCh29-1, which encoded the N-terminal portion of alpha1. A subclone, pCh29-3 (ATCC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP subunits, and in the recombinant prodn. of ABBP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 AspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAspMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGAAAAGAATCAAGTATTAACAACAACAACTTGGCTACAAATGTACTGGACAGATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AsnLeuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 CAAAGGAAGCTGTACAAGGAGCTGCTGAAGAACTACAACCCTCTGGAACGACCAGTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AATGACTCCCAGCCGCTCACTGTCTATTTCACTCTCAGCCTCATGCAGATCATGGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACTTACAGTGGGAATGTGTCTGAATACCCTGGAGTGAAAGAACGTCCGTTTTCCTGATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 CTGATTTGGAAGCCAGATATTCTTCTCTATAACAGTGCTGATGAAAGATTTGATGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIleAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGlyIle
                                                                                                              New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 ArgileTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2769 BP; 790 A; 604 C; 571 G; 804 T; 0 U; 0 Other;
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237
80
127
75
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                    English.
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1179.50
61.08%
45.66%
29.17%
Schoepfer RD
                                                                                                                                                                                                                    Claim 1; Fig 2A-B; 18pp;
                                           WPI; 1997-118297/11.
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Best Local Similarity:
                                                                       P-PSDB; AAW12368
Lindstrom JM,
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17-JUN-1997 (first entry)

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US-09-303-232-2 (1-770)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                   977 ATTGTTGGCCTCTCTGTTGTCACTGTTATCGTTCTACAATACCATCACGATCCA 1036
                                                                                                                                                                                                                                                                                                                               GATGGGGGAAAATGCCTAAATGGACAAGAGTCATCCTTCTGAATTGGTGTGCTTGGTTT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1316 GAGGAAGAAAATCTTCTGCACACTGGCCACCCTCTGAAGGCGACCCAGATTTGGCTAAG 1375
                                                                                                                                                                                                                                                                                                                                                                           CTGAGGATGAAGAGACCAGGG-----GAAGATAAAGTGCGTCCCGCCTGT 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919
                                                               GGGAAGAGAACTGAGAGCTTTTATGAGTGCTGTAAAGAACCATACCCAGATATCACATTC 736
                                                                                                   ACAGTAACCATGAGAACGCAGAACTCTCTACTACGGGCTCAACCTTCTTATTCCCTGTGTA 796
                                                                                                                                            SerieuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThr 571
                                                                                                                                                                                                                                690 ProAspAlaValThrHisHisThrCysIleLysSerSerThrGluTyrGluLeuGlyLeu 709
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                                                                                                                                                                                                                                                                                                         ----TrplleArglleValPheLeuCysTrpLeuProTrplle 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyr 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArgMet 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   710 IleLeuLysGluIleArgPheIleThrAspGlnLeuArgLysAspAspGluCysAsnAsp 729
ThrGlyGlyAspIleSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValPro 491
                                                                                                                                LeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeu 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGTCTTCACCATCATTGTACAATTGGCATCTTAATGTCAGCACCAAACTTTGTA 1552
            -----GCAGATATATCCGGCTATATTTCAAATGGAGAGTGGGGATTTAGTAGGAAATTCCT
                                          GlyLysArgAsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrMetPheAlaIleLeuAlaThrIleAlaValLeuLeuSerAlaProHisIleIle 768
                                                                                    512 AlailelleleArgArgArgThrLeuTyrTyrPhePheAsnLeuIleileProCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 IleAlaAsnAspTrpLysPheAlaAlaMetValValValAspArgLeuCysLeuIleIlePhe
                                                                                                                                                                                                                                                                                                                                                     LeuArgMetSerArgProGlyArgProLeuIleLeuGluPheProThrThrProCysSer
                                                                                                                                                                                                                                                                                                                                                                                               615 AspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLysGluArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                     CAACATAAACAGCGCCGÁTGCAGC-----CTGTCAAGCATGGAGATGAACACTGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLysSerLeuLeu---AlaAsnValLeuAspIleAspAspAspPheArgHis--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1250 GGGGTTCACTGCACACCACCACTGATTCAGGGGTGATC-
                                                                                                                                                                                                                     MetProAlaThrSerAspAlaValProLeu----
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2 cDNA clones (AAT59196 and AAT59197) respectively code for the alphal subunit (AAW12368) and alpha2 subunit (AAW12369) of chick neuronal alphabungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based on the N-terminal amino acid sequence of chicken brain ABBP. The probe alphal. A subclone, pCh29-1, which encoded the N-terminal portion of alphal. A subclone, pCh29-1, which encoded the nescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP
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                                                          Neuronal alpha-bungarotoxin binding protein alpha 2; cholinergic;
ligand binding; ion channel; ss.
Meuronal alpha-bungarotoxin binding protein alpha2 subunit cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 582 A; 406 C; 454 G; 659 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STUDIES
                                                                                                                                                                                                                       location/Qualifiers
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                                                                                                                                                                                                                                                                              /*tag= a
56. 145
/*tag= b
146. 1498
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW12369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
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                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                      Gallus
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284

265 AsnSerSerSerSerSerSerSerAsnSerSerAsnAsnSerSerThrGlnIleLeu

x AAT59197 (1-2101)

2101 244 85 129 109

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.36e-95 1170.50 58.02\* 43.03\* 28.95\*

295 121

--AsnGlyLeuAsnLysHisSerTrpIlePheLeu

285

standard; cDNA; 2101 BP

AAT59197 AAT59197

61

296 LeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArgLeu 315

Watanabe CK, Wood WI; WPI; 2000-572270/53. P-PSDB; AAB24088. 

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Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer. Claim 50; Fig 57; 286pp; English.

The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO1013, PRO1030, PRO1029, PRO1031, PRO1030, PRO1031, PRO1031, PRO1031, PRO1031, PRO1031, PRO1031, PRO1032, PRO1031, PRO1031, PRO1031, PRO1032, PRO1032, PRO1031, PRO1031, PRO1031, PRO1032, PRO1034, PRO1031, PRO1031, PRO1032, PRO1034, PRO1031, PRO1031, PRO1032, PRO1034, PRO1031, PRO1032, PRO1034, PRO2145 OR PRO2034, PRO2034, PRO10317, PRO1031, PRO2145 OR CC PRO10329, PRO334, PRO10317, PRO1031, PRO2145 OR CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds conditions or disorders to be treated with such antibodies and other conditions or disorders to be treated with such antibodies and other conditions or disorders to be treated with such antibodies and other conditions or disorders to extince the process of section of the process of paracreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, conditions or disorders and inflammatory, angiogenic and strongland malignancies, other disorders such as neuronal, glial, estromal and blastocoelic disorders, and inflammatory, angiogenic and hybridistion probes used in the isolation of the human PRO sequences.

AAC58367 to AAC58396 and AAB24087 tepresent human PRO sequences. Process of the human process. present invention

Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

1509 237 82 115 91 Matches: Conservative: Mismatches: Indels: Gaps: Length: US-09-303-232-2 (1-770) x AAC58395 (1-1509) 8.22e-95 1159.50 60.76% 45.14% 28.68% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

201

261

393

321

413

381

433 441 453 501 473 493 612 513 672

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1033 ATGAAGAGGCCCGGGGAGGACAAGGTGCGCCCG---GCCTGCCAGCACAAGCAGCGGCGC 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AanCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPhe 668
                                                                                                                                                     TrpLysProAspValleuMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGln
||||||||||||||||
TGGAAACCAGACATTCTTCTCTATAACAGTGCTGATGAGGGGCTTTGACGCCACATTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         973 GGCAAGATGCCCAAGTGGACCAGAGTCATCCTTCTGAACTGGTGCGCGTGGTTCCTGCAA
||| ||||||| ::: ||||||| TGGAACCATCACCGCACTTCTCCCTGAGCCTCCTGCAGATCATGGACGTGGATGAG
                                                                                                                  553 GCAGATATCAGTGGCTATATCCCCCAATGGAGAATGGGACCTAGTGGGAATCCCCGGCAAG
                                           LysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAspMetAsnLeu
                                                           ArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHisArgIle
                                                                                                                                                                                                            ThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGlyIlePheLys
                                                                                                                                                                                                                            382 ACTAACGIGITGGIGAATICTICTGGGCATIGCCAGIACCTGCCTCCCAGGCATATCAAG
                                                                                                                                                                                                                                                                   SerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArgCysGluMetLys
                                                                                                                                                                                                                                                                                PheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnAspGluThrGly
                                                                                                                                                                                                                                                                                                                                                                              474 GlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              estal cell culture medium for treating cells and for inducing mammaliall lines to conduct calcium ions, comprising specified concentrations ions of sodium, calcium and potassium at specified pH.
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                  TyrArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArg
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transformed cells useful for screening cpds. which modulate activity
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                   single receptor subunits or specific receptor subunit combinations with variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drug
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                                                                                                                                                        identified e.g. screening with cells that express a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 TITGGGTCCTGGTCTTACGGAGGCTGGTCCTTGGATCTGCAGATGCAGGAGG
                                                                                                                                                                                                     Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 0 U; 1 Other;
in normal vs diseased brain tissues.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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DB:
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A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian ocottes, carrying alpha-7 mucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs
                                                                                                                                                                                                                                         used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 ArgirpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHisArgIle 393
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                                                                                                                                                                                                                                        sub-units
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
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Mismatches:
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Matches:
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                                                                     1045 GGCAAGATGCCCCAAGTGGACCAGAGTCATCTTCTGAACTGGTGCGCGTGGTTCCTSCGA
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GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro
                                                                                                                                        985 GGCCTCTCGGTGGTGGTGACGGTGATCGTGCTGCAGTACCACCACCACGACCCCGACGGG
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  PheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGluThrGly 473
                                                                                                     GlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLys 493
                                                                                                                                                                                                                                                                                                                                                                                                                         534 AlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeu 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924
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                                                                                                                                      GCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGAACCTAGTGGGAATCCCCGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 ArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHis---
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                                                                                                                                                                                                              ArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPheAlaIle
                                                                                                                                                                                                                                                                                                                    514 IlelleArgArgArgThrLeuTyrTyrPhePheAsnLeuIleIleProCysValLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysSerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 TyrargThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArg
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                              ----GACTCTGGGGTAGTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetProAspAlaValThrHis-------
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The invention relates to a method for identifying compounds that are artagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ValCysLeuAlaGlyTyrHisGluLys 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NNACHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents cDNA encoding the alpha 7 subunit of the
                                                                                                                                                                                                                      Human neuronal nicotinic acetylcholine receptor alpha 7 subunit
                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                 nn; neuronal nicotinic acetylcholine receptor; nNAChR; flux; alpha 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                 "Human nNAChR alpha 7 subunit"
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Conservative:
Mismatches:
Indels:
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73. .1581
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92US-00938154.
93US-00028031.
93US-00149503.
|||||||::: ::: GCTCCCAACTTCGTG 1554
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                                                                                                  standard;
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30-NOV-1992;
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Pred. No.:
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                                                                                                                                                                               06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elliott KJ,
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                                                                              ABS54875
ID ABS5
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                                                           RESULT
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Db	94 GTCTGGCTGGCGCGCGCGTCGCTCTGCACGTGTCCTGCAAGGCGAGGTTCCAGAGG 153	
δy	314 ArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProValLeuAsnGlu 333	Oy 633 ArgSe
qq	154 AAGCTTTACAAGGAGCTGGTCAAGAACTACATCCCTTGGAGGCCCGTGGCCAATGAC 213	652
Zō qa	334 SerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIleAspValAspGlu 353	1
Sy Db		Oy 669 Tyrai Db 1276
y Qy	ArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleFroProHisArgIle 39 :::          :::	Oy. 689 MetP:            Db 1300 ATGG
ζς Db	TrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGln	Qy 704 GluTy ::: Db 1360 GACCC
S SS	ThrasnvalvalvalargasnasnglySerCysLeuTyrValProProGlyllePheLys	Oy 724 Aspac 
දුරු අධ	434 SerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArgCysGluMetLys 453	Qy 744 LeuC)       Db 1480 CTGT
Oy OD Dp	PheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGluThrGly	Qy 764 AlaPi         Db 1540 GCTCC
Qy Db	474 GlyaspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLys 493 	Search completed: N Job time : 850.783
Qy Dp	494 ArgasnGluileTyrTyrasnCysCysProGluProTyrileAspileThrPheAlaile 513	
Qy Dp	514 IlelleArgArgArgThrLeuTyrTyrPhePheAsnLeuIleIleProCysValLeuIle 533 :::	
Qy	534 AlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeu 553 :::::::::	
Qy Db	554 GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro 573	
Qy	574 AlaThrSerAspAlaValProLeu	
δλ	581 581	
qq	985 GGCCTCTCGGTGGTGGTGACGGTGATCGTGCTGCAGTACCACCACCACGACCCCGACGGG 1044	
Qy Db	582TrpileArgileValPheLeuCysTrpLeuProTrpileLeuArg 596 1045 GGCAAGATGCCCAAGTGGACCAGAGTCATCTTCTGAACTGGTGCGCGTGGTTCCTSCGA 1104	
\$ q	597 MetSerArgProGlyArgProLeulleLeuGluPheProThrThrPro 612	
Qy Db	613 CysserAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLysGlu 632	

Search completed: May 8, 2004, 19:29:44 Job time: 850.783 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 7, 2004, 11:31:03; Search time 18.738 Seconds (without alignments) 3952.801 Million cell updates/sec Run on:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELMLAV.....MFAILATIAVLLSAPHIIVS 770 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nicotinic acetvlch			alpha-bungarotoxin	nicotinic acetylch	alpha 7 neuronal n		hypothetical prote			Ψ										acetylcholine rece	nicotinic acetylch		nicotinic acetylch					
SUMMARIES																														
SUMIN	ΠD	A57175	JN0113	T01378	JH0173	ACHUA7	G02259	S68588	T25671	T19622	T19862	ACFFA1	S12359	A53956	ACFFA2	ACFFIN	A37040	ACCH2N	A40110	ACCHAN	A24572	860589	B37014	T09289	S12899	G02421	ACHUA1	ACBOA1	A28529	A24383
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	Length	502	502	502	511	502	502	498	461	260	542	267	557	503	576	521	502	528	511	456	499	495	512	494	200	498	457	S	457	5
* O	!	29.5	29.5	29.0	28.9	28.7	28.6	27.3	25.0	24.4	24.0	22.0	21.6	20.9	20.9	20.8	20.8	20.7	20.5	20.5	20.4	20.3	20.3	•					19.7	
	Score	1182.5	1179.5	1173.5	1168	vo	1155.5		1009.5		968.5	889	873		843.5	841	840	838	828	827.5	824	N	820.5		806.5		802.5	801	794.5	794
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acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	protein F25G6.4 [i	nicotinic acetylch	nicotinic acetvlch	hypothetical prote	nicotinic acetylch	nicotinic acetylch	hypothetical prote
89	72	18	NN	.74	48	21	05	21	4.	N	r r	4.	99	52	43
I49458	\$13872	A39218	ACCHINI	JH0174	I50548	B35721	S10505	JC4021	E89134	ACCH4N	ACRYA:	T24724	A26456	808162	T23843
2 I494	2 \$1387	2 A392	1 ACCH	2 JH01	2 I505	2 B357	2 8105	2 JC40	2 E8913	1 ACCH	1 ACRYA	2 T2472	2 A2645	2 \$081	2 T238
445 2 I494	7	7	491 1 ACCH	~	7	~	N	N	~	1	Н	~	7	457 2 \$081	565 2 T238
445 2	457 2 8	470 2	П	503 2	461 2	495 2	502 2	627 2	559 2	622 1 1	461 1	468 2	625 2	457 2 8	2
445 2	19.5 457 2 8	470 2	19.5 491 1	503 2	461 2	495 2	19.3 502 2	19.3 627 2	19.3 559 2	19.3 622 1 1	461 1	19.2 468 2	19.2 625 2	457 2 8	19.1 565 2 7

## ALIGNMENTS

RESULT 1 A57175 micotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse C;Species: Mus musculus (house mouse) C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999 C;Accession: A57175 R:Orr-Hitreger, A : Seldin M F : Raldini A : Beaudet A :	7, 1995 1 mapping of the mouse a AS7175; MUD:95324936; Y A	A.Cross-references: GB.L37663; NID:9790853; PIDN:AAC42053.1; PID:9790854 C;Superfamily: acetylcholine receptor C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein	F;1-23/Domain: signal sequence #status predicted <sig> F;2-502/Product: nicotinic acceptor alpha-7 chain, neuronal #status predicted <tr2-54 #status="" (asn)="" (covalent)="" (thr)="" (tyr)="" <tr2-5;26-317="" <tr2-5;262-280="" <tr3-5;40-488="" <tr3-5;413-47="" binding="" carbohydrate="" domain:="" f;355,413-47="" f;442="" phosphate="" predicted="" predicted<="" site:="" th="" transmembrane=""><th>Query Match 29.2%; Score 1182.5; DB 2; Length 502; Best Local Similarity 45.8%; Pred. No. 5e-77; Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;</th><th>Qy 297 IYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDB 353                                       </th><th>OY 354 KNOLLVTNVWLKLEWNDMYLRWNTSDYGGYKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413                                       </th><th>QY 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDBTG 473                                       </th><th>QY 474 GDISSYVLNGEWELLGVPGKRNBIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533                                      </th><th>Qy 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581 :::                                    </th></tr2-54></sig>	Query Match 29.2%; Score 1182.5; DB 2; Length 502; Best Local Similarity 45.8%; Pred. No. 5e-77; Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;	Qy 297 IYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDB 353	OY 354 KNOLLVTNVWLKLEWNDMYLRWNTSDYGGYKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413	QY 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDBTG 473	QY 474 GDISSYVLNGEWELLGVPGKRNBIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533	Qy 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581 :::
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Query Match  29.2%; Score 1179.5; DB 2; Length 502;  Best Local Similarity 45.7%; Pred. No. 8.2e-77;  Matches 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9;  Qy 295 LLIYLNISAKVCLAGYHEKRLHDLLDPYNTLERPVLNSDPLOLSFGLTLMQIDDV 351	Qy 472 TGGDISSYVLNGEWELLGVECKRNEIYYNCCPEFYIDITE Db 185ADISGYISNGEWDLYGIPGRKTESFYECKEPPYDITE Qy 532 LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNAVABI Db 243 LISALALVFLLPADSGEKLSLGTTLLSLTVFLLVABI Db 243 LISALALVFLLPADSGEKLSLGTTVLLSLTVFLLVABI DD 303 IVGLSVVTVIVLQYHHHDPDGGKMFKWTRVILLNWCAWF  Qy 615 DTSSERKHQILSDVELKERSSKSLL-ANVLDIDDDFRH DD 358 QHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLL Qy 670 RTVYGQGDDGSIGPIGSTRMPDAVTHTCIKSSTEYELGI  Qy 670 RTVYGQGDDGSIGPIGSTRMPDAVTHTCIKSSTEYELGI  Qy 670 RTVYGQGDDGSIGPIGSTRMPDAVTHTCIKSSTEYELGI  GY 670 LTVYGQGDDGSIGPIGSTRMPDAVTHTCIKSSTEYELGI	Oy 730 IANDWKFAANVUDELCIIFTMFAILATIATIATIATISTHE FOR THE FOLLOWING A 456 ICNEMKFAANVUDELCIIFTMFAILATIATIATISTHE FOR THE FOLLOWING A 56 ICNEMKFAANVUDELCIIFTMFAILATIATISTHE FOR THE FOR THE FOLLOWING A 56 ICNEMKFAANVUDELCIIFTMFAILATICTIGILMSAPNFV 494  BY 101378  C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000 C, Accession: T01378  R.Sequela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.  G.Saquela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.  A. Neurosci. 13, 596-604, 1993  A. Title	Query Match   29.0%; Score 1173.5; DB 2; Length 502;
OY  S82	Σ λ λ	ster, J sptor F sptor, F sptor, J sptor	130/3 receptor; phos n, neuronal #s predicted #status predicd d

	Db 187 DLQMLEADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRILYYGL 243  Qy 525 NLIIPCVLIASMALIGFTLPPDSGEKLSLGYTLLISLTVFLNAVAETWRATSDAVPL 581  244 NLIIPCVLIASSAALIGFTLPPDSGEKISLGYTLLISLTVFLLNAAETWRATSDSVPLIAQ 303  Qy 582
	RESULT 5 ACHUA7 Achinic acetylcholine receptor alpha-7 chain precursor, neuronal - human N:Alternate names: choline-receptor alpha-7 chain
RESULT 4 JH0173 alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999 C;Accession: JH0173 R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of this A;Reference number: JH0172: MIJD:9031518: PMID:246519	C;Species: Homo sapiens (man) C;Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999 C;Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999 C;Accession: 137185; A54194; S603309 R;Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J. Mol. Pharmacol. 45, 546-554, 1994 A;Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the omers expressed in Xenopus occytes. A;Reference number: 137185; MUID:94195283; PMID:8145738 A;Accession: 137185 A;Accession: 137185 A;Andownlotter and from GB/EMBL/DDBJ
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asynaptic pseudodend	A;Reference number: A54194; MUID:94245214; PMID:8188270 A;Reference number: A54194; MUID:94245214; PMID:8188270 A;Recession: A54194 A;Molecule type: mRNA A;Residues: 24-363,'S',365-374,'A',376-408,'AWDAP',414-502 <chi>A;Cross-references: GB:Z23141; NID:9457736; PIDN:CAA80672.1; PID:9457737 A;Experimental source: retina</chi>
	C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized C;Genetics: A;Gene: GDB:CHRNA7 A;Gene: GDB:CHRNA7 A;Cross-references: GDB:138751; OMIM:118511
Query Match 28.9%; Score 1168; DB 2; Length 511; Best Local Similarity 44.2%; Pred. No. 5.6e-76; Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;	A;Note: defects in this gene have been associated with mental retardation and schizophre C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains ar C;Superfamily: acetylcholine receptor
285 NGINKHSWIFLLIYLNLSAKVCLAGYHEKRLIHDILDPYNTLERPVINESDPLQLSFGLT 344 :   :   :	C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor; F:1-23/Domain: signal sequence #status predicted <sig>F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted F:231-254/Domain: transmembrane #status predicted <fr1></fr1></sig>
345 LMQIIDVDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404  :	F;262-280/Domain: transmembrane #status predicted <pr2> F;296-317/Domain: transmembrane #status predicted <pr3> F;470-488/Domain: transmembrane #status predicted <pr4> F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted</pr4></pr3></pr2>
405 DEGEDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDGRCEMKFGSWTYDGFGL 464	F;150-164/llsuLinde Donds: #status predicted F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted F;415/Binding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
465 DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 524	Query Match Best Local Similarity 45.1%; Pred. No. 1.9e~75;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;	qa	185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI 244
297 IYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353 ::	ζό O	534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL 581 :::
354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413	λ <sub>O</sub>	582
414 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473    : ::   :	oy da	613 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAF 668  1
474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533 	λό qa	669 YRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRK 723 
534 ASMALIGETLPPDSGEKLSLGVTILLSLTVFLNMVÄETMPÄTSDAVPL 581 :::	ço du	724 DDECNDIANDWKFAAMVVDRLCLIFTWFAILATIAVLLSAPHII 768
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613 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPWTPGGTLPHNPAF 668	C; Specie C; Date: C; Access	מה בי
669 YRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRK 723 402DSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449	R;Balliv J. Mol. A;Title: A;Refere	et, M.; Allod, C.; Bertrand, S.; Bertrand, D. Biol. 258, 261–269, 1996 Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. nce number: 868587; MUID:96196478; PMID:8627624
724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 769    : ::	A; Access A; Status A; Molecu A; Residu	: nucleic acid sequence not shown le type: mRNA sel 1-498 cBAL>
RESULT 6 G02259 alpha 7 neuronal nicotinic acetylcholine receptor - human	C;Superf C;Keywor F;1-19/D F;20-498	C;Superfamily: acetylcholine receptor. C;Superfamily: acetylcholine receptor. C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane, F;1-19/Domain: signal sequence #status predicted <sig> F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <mat;< td=""></mat;<></sig>
ories: Homo sapiens (man) e: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999 ession: G02259 nard, S.	Query Match Best Local Matches 22	/ Match Local Similarity 43.3%; Pred. No. 2.1e-71; nes 227; Conservative 76; Mismatches 139; Indels 82; Gaps 8;
submitted to the EMBL Data Library, November 1995 A;Reference number: H00936 A;Accession: G02259 A;Status: preliminary; translated from GB/EMBL/DDBJ	yo da	295 ILIYLNISAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
ecule type: mRNA ecule cype: Lebo> sss_references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077 erfamily: acetylcholine receptor	VQ Op	355 NQLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIMKPDVLMYNSADEGFDGTYQT 414   ::                       : ::    :    :
Query Match  28.6%; Score 1155.5; DB 2; Length 502; Best Local Similarity 45.1%; Pred. No. 4.3e-75; Matches 237; Conservative 80; Mismatches 117; Indels 91; Gaps 12;	λό QΩ	415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474  :: : : : :  :       :
297 IYLNLSAKVCLAGYHEKRLIHDLIDPYNTLERPVLNESDPLOLSFGLTLMQIIDVDE 353 ::   :	λ O	475 -DISSYVINGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFRNIIPCVLI 533      -
354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413 	ço d	534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETMPATSDAVPL 581  244 TLMTLGFTLPPDAGEKITLQITVLLSICFFLSIVSEMSPPTSEAVPLGIFFTCCMIVV 303
414 TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473	<b>&amp;</b> 43	582
474 GDISSYVLNGEWELLGVPGKRNEIXYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI 533	<sup>ر</sup> ة	617 SSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNP 666 : :

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                                                   --NGLTSLGSIPSTMISSNGTTTDVSQQATLLILHRIYHELKIVTKRMIEG 453
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C;Species: Caenorhabditis
C;Species: T25671
A;Reference number: Z20067
A;Reference number: Z20067
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor
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Rikershaw, J.

Rikeference number: 219153

A; Accession: T19622

A; Accession: T19622

A; Accession: T19622

A; Molecule type: DNA

A; Residues: 1-560 < WIL>

A; Residues: RMBL: 293778; PIDN: CAB07843.1; GSPDB: GN00019; CESP: C31H5.3

C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 VSILIWETKCSKVIWTGDHERRLYAKLAENYNKLARPVRNESEAVVVLLGMDYQQILDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 PVNAVVLYTGNVTWIPPAIIRSSCAIDIAYFPFDTQHCTMKFGSWTYSGFFTDL---INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ISSLALLSFTLPADCGEXLNLGVTIFMSLCVFWIMVAEAMPQTSDALPL-IQIXFSCIMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISPATÝKPNGEWELLGLTSQRSIFFYECCPEPYYDVTFTVSIRRTLYYGFNLLLPCML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 QTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SDVELKERSSKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 GGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVL
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                 Length 560;
                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C;Superfamily: acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                             24.4%; Score 988; DB 2; L. 37.2%; Pred. No. 5.2e-63; ive 85; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
- Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 735 KFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 MFASRVVDRVCFLAFSAFLFMCTAIISYNAPHLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 CANN-----OKTOFEDRHFHH-
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 37.2;
Matches 214; Conservative
hypothetical protein C31H5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 SDTSSERKHO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      639 LANVLD-
                                                                                                                                                                                                                                                                              A; Gene: CESP: C31H5.3
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T19862 hypothetical protein C40C9.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000 C;Accession: T19862

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A;Ctoss-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A;Note: 538-Tyr was also found
C;Genetics:
A;Gene: FlyBase:nAcR-alpha-96Aa
A;Gene: FlyBase:nAcR-alpha-96Aa
A;Gene: FlyBase:nAcR-alpha-96Aa
A;Gross-references: FlyBase:FBGn000036
A;Map position: 3R 96A
A;Map position: Application creceptor alpha-like chain #status predicted <RX7-
F;22-240/Domain: extracellular #status predicted <RX7-
F;240-264/Domain: transmembrane #status predicted <TWA->
F;36-515/Domain: intracellular #status predicted <TWA->
F;36-515/Domain: transmembrane #status predicted <TWA->
F;36-515/Domain: transmembrane #status predicted <TWA->
F;314-532/Domain: intracellular #status predicted <TWA->
F;45-233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;149-163,222-223/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Si2359

Micotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C;Species: Schistocerca gregaria (desert locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: S12359
R;Marshall, J; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G., EMBO J. 9, 4391-4398, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 YTVNLIIPCVGISFLSVLVFYLPSDSGEKISLCISILLSLTVFFLLLABIIPPTSLTVPL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 LGKYLLFTMMLVTLSVVVTIAVLNVNFRSPVTHRMAPWVQRLFIQILPKLLCIERPKK-- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TVYGQGDD-----GSIGPIGSTRMPDAVTH 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTCIKSST-----EYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QLQD----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLY 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KQTADSDNIEVGIDLQDYYISVEWDIMRVPAVRNEKFYSCCEEPYLDIVFNLTLRRKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 GTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 ILEFPTTPCSDTSSERKHOILSDV-ELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 SWIFLLIYLNLS-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Mismatches 168; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 567;
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Pred. No. 6.6e-56;
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35.2%;
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Best Local Similarity 35.24
Matches 196; Conservative
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C; Species: Drosophila melanogaster
C; Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
C; Accession 500381; A38801
B; Bossy, B; Ballivet, M.; Spierer, P.
EMBO J, 7, 611-618, 1988
A; Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to ver A; Accession: S00381; MUD:88283626; PMID:2840281
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: MOSS
A; MOSS
A; Molecule type: MOSS
A; Molecule type: MOSS
A; Molecule type: MOSS
A; 
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         R;Hembry, C.
submitted to the EMBL Data Library, March 1996
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19862
A;Accession: T19862
A;Accession: T19862
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-542 < WIL>
A;Cross-references: EMBL: Z70266; PIDN: CAA94206.1; GSPDB: GN00028; CESP: C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: X
A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 EKRILHDILDPYNTLERPVINESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDM 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : | : | : | | : | 382 KAREKAKQGSIKNGVGPGKPTDSVHPSEGLSLMKNIKLGRQQTIDFEYEFHVQHNHLMPV 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 NLRWNTSDYGGVKDLRIP--PHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 KLKWDPSEYGGIKDIRIPGNANAIWKPDVLLYNSADENFDSTYPVNYVVSYTGDVLQVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQ-----DETGGDISSYVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 VVFTVLVLNLHNRKPETHEMSPFLRELLLIMLPWLLLLMSRPGKTIF-----NCTHLKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 APSEMTP-----RVTY-----SKVMAESYVEDVVMTELNKYMQKACLELKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIASMALLGFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.0%; Score 968.5; DB 2; 38.7%; Pred. No. 1.2e-61; ive 79; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 208; Conserv
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DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNLIIPCVLIA 355 NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT Gaps A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Residues: 30-503 <ANA>
A;Cenetics: MBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics: A;Gene: GDB:HRNA3
A;Gene: GDB:HRNA3
A;Gene: GDB:HRNA3
A;Map position: 15q24-15q24
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor 64; Length 503; Indels SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-Query Match
20.9%; Score 845; DB 2; Le
Best Local Similarity 35.2%; Pred. No. 8.1e-53;
Matches 178; Conservative 97; Mismatches 166; 315 LSIVITVFVLNVHYRTPTTHTMPSWVKTVFLNLLPRVM---762 |||:||: | :||: || :|| AMVIDRIFLWVFTLVCILGTAGLFL 494 AMVVDRLCLIIFTMFAILATIAVLL A; Molecule type: mRNA 195 475 535 582 363 678 470 임 ò d à ò 요 ò a ð 셤 à 셤 Š 셤 8 셤 δ 굄 A; Residues: 1-557 mans.

A; Residues: 1-557 mans.

A; Residues: 1-557 mans.

A; Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134

A; Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134

C; Superfamily: acetylcholine receptor
C; Reywords: g1ycoprotein; on channel; neurotransmitter receptor; transmembrane protein
C; Reywords: g1ycoprotein; on channel; neurotransmitter receptor alpha-Li chain #status predicted <NISF; 24-557, Product: nicotinic acetylcholine receptor alpha-Li chain #status predicted <MAI
F; 245-266, Domain: transmembrane #status predicted <TM1>
F; 308-329, Domain: transmembrane #status predicted <TM3>
F; 308-329, Domain: transmembrane #status predicted <TM4>
F; 308-329, Domain: transmembrane #status predicted <TM4>
F; 318-329, Domain: transmembrane #status predicted <TM4>
F; 325, Domain: transmembrane #status predicted <TM5 nicot neuronal A,Title: Sequence and functional expression of a single alpha subunit of an insect A,Reference number: S12359; MUID:91092263; PMID:1702381
A;Accession: S12359
A;Molecule type:\_mRNA\_ nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human ("Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 20-Aug-1999
C'Accession: A53966, 521338
R'Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A,Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a man and a man a 8; 293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD 352 EKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTY 412 QTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL----QL 468 128 MTKAVLHHTGKVVWTPPALFKSSCEIDVRYFPFDQQTCFMKFGSWTYDGDQIDLKHINQK 187 QDE----TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 524 581 607 364 652 --CRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLI 710 475 67 -WIRIVFLCWLPWILRMSRPGRPLILE NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---308 YLLFTMVLVGLSVVITIMVLNVHYRKPSTHKMAPWVRKVFIRRLPKLLLMRVPEQLL---QLHHLQRPGGCNGLHSATNR--FG-GSAGAFGGLPSVVGLDGSLSDVATRKKYPFELEKA Gaps 530 LKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAP 765 FPTTPCSDTSSERKHQILSDVELKERSSKSLLA----NVLDIDDDFRHN-----74; Length 557; 90; Mismatches 174; Indels ; DB 2; ] 9.1e-55; 21.6%; Score 873; 36.8%; Pred. No. 9 Conservative Similarity Status: preliminary Molecule type: mRNA A;Accession: A53956 A;Status: prelimina Local Simi hes 197; 188 89 469 248 608 353 413 525 582 365 653 711 Query Match Best Loca Matches RESULT 13 A53956 d δ qq g  $\delta$ g g ð gg δ ΩD à g  $\delta$ q à ð à

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nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanog C; Species: Drosophila melanogaster
C; Species: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 21-Jun-2002
C; Date: 31679; 510366; 511084
R; Sawruk, B.; Schloss, P.; Betz, H.; Schmitt, B.
BMBO J. 9, 2671-2677, 1990
A; Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel dev A; Reference number: S11679; MUD: 90360975; PMID: 1697262
A; Accession: S11679.
submitted to the EMBL Data Library, June 1990
A.bescription: Wucleotide sequence of the mature human nicotinic acetylcholine receptor
A;Reference number: $21338
A;Accession: $21338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 NQIMETNLWLKQIWNDYKLKWNPSDYGGABFMRVPAQKIWKPDIVLYNNAVGDFQVDDKT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FMTRPTSNEG 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | | | : | : | : | | NAQKPRPLYGABLSNILNCFSRAES------KGCKEGYPCQDGMCGYCHHRRIKISNF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 SANLTRSSSSESVDAVLS----LSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGD
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A; Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A; Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A; Note: 232-II was also found
R; Baumann, A.; Jonas, P.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 3640, 1990
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A;Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R;Anand, R.; Lindstrom, J.
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530 WLFMIASLVGTFVILGEAPSL 550
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                                                                                                                                                                                                                                                                                                                     A; Recession: S11084
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 42-90, 1', 92-576 <JON>
C; Genetics:
A; Genetics:
A,Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acety
A,Reference number: S10306; MUID:90301489; PMID:2114015
A,Accession: S10306
                                                                                                                                                            A,Cross-references: EMBL:X52274; NID:97802; PIDN:CAA36517.1; PID:97803
R;Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, B.D.
FEBS Lett. 269, 264-268, 1990
A;Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel A;Reference number: S11084; MUID:90353591; PMID:2117557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLKHISQKNDKDNKVEIGIDLREYYPSVEWDILGVPAERHEKYYPCCAEPYPDIFFNITL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 HSW----IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DL----QLQD-----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPAT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----WIRIVFLCWLPWILRMS 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLALPLIGKYLLFTMLLVGLSVVITIIILNIHYRKPSTHKMRPWIRSFFIKRLPKLLLMR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKE----RSSKSLLANVLDIDDDFRHNC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 MQMNSGGSSPDSLRRMQGRVGAGGCNGMHVTTATNRFSGLVGALGGGLSTLSGYNGLPSV 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VT-----HHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 111;
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Best Local Similarity 34.4%
Matches 193; Conservative
                                                                                                  A; Molecule type: mRNA
A; Residues: 1-576 <BAU>
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nicotinic acetylcholine receptor nonalpha chain precursor - fruit fly (Drosophila melano (Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999 C;Accession: 803012; A38064; Ā26313; A28126; A38759 R. Ascession: 803012; A38064; Ā26313; A28126; A38759 R. B. D. FEBS Lett. 235, 40-46, 1988 A. Title: Characterization of an invertebrate nicotinic acetylcholine receptor gene: the A;Reference number: 803012; MUID:88296842; PMID:3136037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues 1-521 < csaw>
A, Cross-references: BMBL:X07956; NID:g7602; PIDN:CAA30778.1; PID:g1065712
A, Accession: A38064
A, Accession: A38064
A, Bood and a company and a
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A, Residues: 1-72, VV, 74-521 cHER>
A, Cross-references: EMBL:XO4016; NID:97537; PIDN:CAA27641.1; PID:97538
R, Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
R, Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
A) Title: Expression of a Drosophila melanogaster acetylcholine receptor-related gene in
A, Reference number: A28126; MUID:88174720; PMID:2832736
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A.Mar position: 31. 64B/C

A.Mar position: 31. 67/3; 19/2; 25/3; 467/3

A.Mintrons: 22/1; 67/3; 19/2; 25/3; 467/3

C.Superfamily: acetylcholine receptor

C.Reywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane

C.Reywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane

Fit 124/Domain: signal sequence #status predicted <SIG>
F;25-51/Product: nicotinic acetylcholine receptor nonalpha chain #status predicted <AMT>
F;25-51/Product: nicotinic acetylcholine receptor nonalpha chain #status predicted <AMI>
F;26-286/Domain: transmembrane #status predicted <TM2>
F;302-33/Domain: transmembrane #status predicted <TM3>
F;324-481/Domain: intracellular #status predicted <TM3>
F;348-500/Domain: transmembrane #status predicted <TM4>
F;482-500/Domain: transmembrane #status predicted <TM4>
F;482-166/Domain: transmembrane #status predicted <TM4>
F;482-166/Disulfide bonds: #status predicted
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A;Cross-references: FlyBase:FBgn0000038
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Best Local Similarity 35.6%;
Matches 186; Conservative 9
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A,Residues: 1-521 <WAD>
A,Cross-references: EMBL:M20316
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245	- 576	305	r 611	1365	1 664	. 423	724	1 462			
187 NKNFVDLSDYWKSGTWDIIEVPAYLN-VYEGDSNHPTETDITFYIIIRRKTLFYTVNLIL 245	529 PCVLIASMAILGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATS	246 PTVLISFLCVLVFYLPAEAGEKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLF 305	DAVPLWIRIVFLCWLPWILEN	6 TFIMNTVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLFMKRPRKTRLRMMMEM 365	612 PCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664	366 PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL	NPAFYRTVYGQGDDGSIGPIGSTRMDDAVTHHTCIKSSTFYBLGLILA	4GLGDGCRRESESSDSILLSPEASKATEAVEFIAEHLRNE	725 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI 767		
18.	52	24	577	306	613	366	999	424	725	46	
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Search completed: May 7, 2004, 11:39:30 Job time : 20.738 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 11:18:28; Search time 14.3803 Seconds (without alignments) 2788.120 Million cell updates/sec May Run on:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ы	P49582 mus musculu	2770 gall	rattus	homo sa	pos	caer	P09478 drosophila		P23414 schistocerc		homo				10	gallus	rattus	P04757 rattus norv		P18845 carassius a	drose	homo sa	gallı	bos tan	homo	mus musc	P05377 xenopus lae	143 rattus n	ਯ	08 rattus	P26153 qallus qall	9484 gallus	4 mus mus
SUMMARIES	ID	ACH7 MOUSE	ACH7 CHICK	ACH7 RAT	ACH7 HUMAN	ACH7 BOVIN	ACH1_CAEEL	ACH1 DROME	ACH1 MANSE				- 1	- 1	ACH2 CHICK		ACH3_CHICK		ACH3_RAT			ACH4_DROME	ACHP HUMAN	ACH6_CHICK	ACHA_BOVIN	ACH6_HUMAN		ACH2_XENLA				ACHP CHICK	ACHN CHICK	ACH4_MOUSE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=11097796; PubMed=1702646; Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-CCT-2003 (Rel. 42, Last amoctation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
          POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                             (b) SIGLAGATI).

N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
C9312E5226D120E3 CRC64;
                                                                                                                                                                                        85;
                                                                                                                                                              29.2%; Score 1182.5; DB 1; Length 502; 45.8%; Pred. No. 5.1e-75; ive 80; Mismatches 118; Indels 85;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                 "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
MEDLINE=85270494; PubMed=3860855;
Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
uronal nicotinic acetylcholine receptor subunit (alpha 7) is opmentally regulated and forms a homo-oligomeric channel blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22049732; PubMed-1719423;
Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
"Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
MEDLINE=93024917; PubMed=1383829;
Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
Changeux J.-P., Bertrand D.;
Mutations in the channel domain of a neuronal nicotinic receptor
convert ion selectivity from cationic to anionic.";
Nature 359:500-505 (1922).

1-- FINCTION: After binding acetylcholine, the AChR responds by an
extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                            Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J.; "Brain alpha-bungarctoxin binding protein cDNAs and Mabs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                        Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-18 FROM N.A.
STRAIN=White leghorn; TISSUE=Erythrocyte;
                                                                                                                                              MEDLINE=90315158; PubMed=2369519;
                                                                                                                                                                                                                                                                                                                             MEDLINE=93049204; PubMed=1425587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52295; CAA36543.1; -. EMBL; X68246; CAA48317.1; -. EMBL; X68586; CAA48576.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 11:4529-4538(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinic receptor.";
Nature 353:846-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF LEU-270.
                                                              Neuron 5:847-856(1990).
                                                                                                                                                                                                                                              Neuron 5:35-48(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins.
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                                                                                                        SEQUENCE FROM N.A.
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                                             alpha-BTX
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      neuronal
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PDR; JN0113; JN0113. PDB; 1KC4; 17-APR-02.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 DTSSERKHQILSDVELKERSSKSLL-ANVLDIDDDFRH----NCRPMTPGGTLPHNPAFY 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670 RTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECND 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ADISGYISNGEWDLVGIPGKRIESFYECCKEPYPDITFIVIMRRRILYYGLNLLIFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                       295 LLIYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     532 LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                    NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
L->S, T: SUPPRESSES INHIBITION BY THE
                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                75;
PDB; 1KL8; 17-APR-02.

InterPro; IPR006203; Neu_channel_memb.

InterPro; IPR006202; Neu_chan_LBD.

InterPro; IPR006201; Neur_chan_LBD.

Pfam; PP02931; Neur_chan_EBD; 1.

Pfam; PP02932; Neur_chan_memb; 1.

PRINTS; PR00252; NRIONCHANNEL.

IIGRFAMS; TIGRO0860; LIC; 1.

PROSITE; PS00236; NBUROTR ION_CHANNEL; 1.

POSTSYNAQLIC membrane; Johic Channel; Glycoprotein; Signal; Iransmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                     29.2%; Score 1179.5; DB 1; Length 45.7%; Pred. No. 8.2e-75; ive 80; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                       OPEN-CHANNEL BLOCKER QX-222.
QR -> ET (IN REF. 3).
572325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       730 IANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                                 ALPHA-7 CHAIN
EXTRACELLULAR
                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                              CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                    27 QI
56946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               237; Conservative
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2555
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502 AA;
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DISULFID
DISULFID
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CARBOHYD
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                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Multigene family.
SIGNAL 1 22 BY SIMILARITY.
CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                          MEDLINE=93147931; PubMed=7678857; Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.; "Molecular cloning, functional properties, and distribution of rat brain alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartley M., Substitute of AUG-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                          01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0860; LLC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Postsynaptic miltidene family.
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
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 502 AA.
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PIR; T01378; T01378.
InterPro: IPR006029; Neu channel memb interPro: IPR006020; Neur chan LBD.
InterPro: IPR006201; Neur chan LBD.
Pfan; PP02931; Neur chan LBD; 1.
Pfan; PP02932; Neur chan LBD; 1.
PRINTS; PR00522; NATGNOGANNEL.
                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Brain;
                             01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                              Neurosci. 13:596-604(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S53987; AAB25224.2; -.
                                                                                                             Rattus norvegicus (Rat).
STANDARD;
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                                                                                                                                                               NCBI_TaxID=10116;
                                                                                              CHRNA7 OR ACRA7.
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Logel J., Drebing C., Barnhart M., Antle C., Leonard S., Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
          TISSUE=Hippocampus;
SEQUENCE FROM
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                                                                                                                                                                                                              414 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                                         SALALLVFILPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94195283; PubMed=8145738; Mend R., Lindstrom J.; Perg X., Katz M., Gerzanich V., Anand R., Lindstrom J.; Perg X., Gerzanich V., Anand Peng X.; Katz M., Gerzanich V., Anand Linds a libha J. acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SYSY cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Kanopus oocytes "; Mol. Pharmacol. 45:546-554 (1994).
                                                                                                                            297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                   CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV
                                                                                                                                                                                                                                                                                                                                                                                                          -- PPTSNGNLLY -- IGFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                           393 EGMHCAPTPDSGVVCGRLACSPTHDEHLMHGAHPSDGDPDLAKILEEVRYIANRNRCQDE
                                                                                                                                         ----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                               305 GLSVVVTVIVLRYHHHDPDGGKMPKWTRİİLLNWCAWFLRMKRPGEDKVRPACQHKPRR-
                                                                                                                                                                                                                                                                                                                                                                                                                               673 YGQ-----GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDE
                                                                                                                                                                                                                                                          GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                 534 ASMALLGFTLPPDSGEKLSLGVTIILSLTVFLNMVAETMPATSDAVPL------
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH7_HUMAN STANDARD; PRT; 502 AA.
P36544; O15626; Q96RH2; Q99555; Q9BXH0;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N -> F (IN REF. 2).
P -> R (IN REF. 2).
                                                                                                        85;
                                                                                   DB 1; Length 502;
                                                                                            ; Pred. No. 2.1e-74;
80; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEVICSEWKFAACVVDPLCLMAFSVFTIICTIGILMSAPNFV 494
                                                               00996E74EC7B9A56 CRC64;
  SIMILARITY)
                                                                                    29.0%; Score 1173.5;
                                                                                                                                                                                                                                                                                                                                                                                                          ----LASVELSAGAG--
  BY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                56410 MW;
                                                                                              45.68:
                                                                                                         Conservative
            46
90
133
447
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            46
90
133
447
469
502 AA;
                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHRNA7 OR NACHRA7
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                                                                                                                                                                                                                                                                                                                                                                                                           CS-
                                                                                                       Matches 238;
                                                                                                                                                                                                                                                                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                       245
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                                          CONFLICT
CONFLICT
SEQUENCE
                     CARBOHYD
                                                                                                                                                                                          68
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            CARBOHYD
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MEDLINE=97162233; PubMed=9009220; Groot Kormelink P.J., Luyten W.H.M.L.; Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32."; FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and chromosomal localization of the human alpha 7-nicotinic receptor subunit gene (CHRNA7).";
Genomics 19:379-381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 118-129 FROM N.A. MEDLINE-21818878; PubMed-11829490; Riley B., Williamson M., Collier D., Wilkie H., Makoff A.; "A 3-Mb map of a large segmental duplication overlapping the alpha7-nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14."; Genomics 79:197-209(2002).
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SEQUENCE FROM N.A.

MEDILINE=97062879; PubMed=8906617;

Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Ohnson E.C., Velicelebi G., Harpold M.M.;

"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herath A.,
Page M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94245214; PubMed-8188270;
Chini B., Raimondi B., Elgoyhen A.B., Moralli D., Balzaretti M.,
Helnemann S.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cluster analysis of an extensive human breast cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M. Lee J., Tian J., Giordano T.;
"Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Epidermal keratinocytes;
Arredondo J., Grando S.A.
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=21829512; PubMed=11840567;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L.,
Parekis R., Waterfield M.D., O'Hare M.J., Neville M.A.,
Zvelebil M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein expression map database.";
Proteomics 2:212-223(2002).
                                                                                                                                                                                                                                                                                                          Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drug Dev. Res. 30:252-256(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 24-502 FROM N.A.
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245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                                                     305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNMCAWFLRMKRPGEDKVRP-ACQHKQRR 363
                                                                                                                                                                                                                                                                                                                                                                           CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
KNQVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By similarity). Homo-oligomer of the short form gives rise to unfunctional channels, as does coexpression of both long and short
                                                                                                                                               185 ADISGYIPNGEMDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRTLYYGLNLLIPCVL.
                                                                                                                       474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                           -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromaffin cells: molecular cloning, functional expression and alternative splicing of the alpha 7 subunit.";

Bur. J. Neurosci. 7:647-655(1995).

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isold=P54131-2; Sequence=VSP 000075; TISSUE SPECIFICITY: At least in chromaffin cells. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Adrenal medulla, MEDLINE=95346009; PubMed=7620615; MEDLINE=95346009; PubMed=7620615; Gampos-Caro A., Stuehmer W., Gutierrez L., Criado M., Gutierrez L., Criado M., Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
                                                                                                                                                                                                          534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                                                                                                                                                                                    364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724 DDECNDIANDWKFAAMVVDRLCLIIFTMFALLATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
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NCBI TaxID=9913;
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Transmembrane; Louis BY SIMILARITY.
SIGNAL 1 22 BY SIMILARITY.
SIGNAL 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
ALPHA-7 CHAIN.
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MASS SPECTROMETRY: MW-54157.68; METHOD=MALDI.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
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Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> G (IN REF. 1 AND 7).
S -> N (IN REF. 2 AND 6).
S -> P (IN REF. 2 AND 6).
C -> S (IN REF. 8).
A -> G (IN REF. 1).
RMACS -> AWPAP (IN REF. 8).
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82; Mismatches 115; Indels
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EMBL; Y08420; CAA69697.1; --
EMBL; AF788585; AAK68111.1; --
EMBL; L25837; -; NOT ANNOTATED_CDS.
EMBL; A733278; AAK19515.1; --
PIR; G02259; G02259; EIR; I37185; ACHUA7.
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MIM; 118511; -.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 499;
                                                                                                                                                                                                                                                    Postsynaptic membrane, Ionic Channel; Glycoprotein; Signal; Transmembrane; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1157; DB 1; Length 49
Pred. No. 3e-73;
5; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POI
Missing (in isoform Short).
/FTId=VSP_000075.
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                                                                                                                                                                                                                                                                                                          ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
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POTENTIAL.
BY SIMILARITY.
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                                                                                                                                                                                                                                         CHANNEL; 1
                                                                                                                                   InterPro; IPR006629; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONFIANNEL.
TIGRPAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
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46.4%; Pred
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405 GRVACSPTHDEHLLHAGQPSEGDPDLAKILEEVRYIAHRFRCQDESEAVCSEWKFAACVV 464
                                                                                                                                                                                                                                             Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                  ., Bertrand D.;
in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUNETION: POSSIBLE acetylcholine receptor.
- FUNCTION: POSSIBLE acetylcholine receptor.
- SUBCELLULAR LOCATION: Integral membrane protein.
- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X33887; CAA58764.1; -.

R PIR; S66588; G8588.

R HSSP, P58154; 119B.

R HORPPO; P58154; 119B.

R InterPro; IPR006029; Neu_channel_memb.

R InterPro; IPR006020; Neur_channel.

R InterPro; IPR006201; Neur_channel.

R Pfam; PF02331; Neur_chan memb; 1.

R Pfam; PF02332; NRIONCHANNEL.

R Pfam; PF02332; NRIONCHANNEL.

R TICRFAMS; TICRN0860; LIC; 1.

R RECEPLOY: POSESYNAPTIC membrane; Ionic channel; Glycoprotein; manney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
F25G6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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EXTRACELULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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BY SIMILARITY.
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                               742 DRLCLIIFTMFAILATIAVLLSAPHII 768
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DRLCLMAFSVFTILCTIGILMSAPNFV
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=96196478; PubMed=8627624;
Ballivet M., Alliod C., Bertrand S.,
"Nicotinic acetylcholine receptors in
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                elegans.";
J. Mol. Biol. 258:261-269(1996).
                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 ILMILLGFILPPDAGEKITLQITVLLSICFFLSIVSEMSPPTSEAVPLLGIFFTCCMIVV 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IDDDFRHNCRPMTPGGTLPHNP 666
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                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                               295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                            LLISCAILAAPTLGSLQERRLYEDLMRNYNNLERPVANHSEPVTVHLKVALQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                            415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=88283626; PubMed=2840281;
Bossy B., Ballivet M., Spierer P.;
"Conservation of neural nicotinic acetylcholine receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACHI DROME STANDARD; PRT; 567 AA.

10.9478; Q9VC74;

10.-CCT-2003 (Rel. 10, Created)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
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10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Last sequence update)
10.-CCT-2003 (Rel. 42, Las
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                                                                                        Length 498;
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  93 N-LINKED (GLCNAC. . .) (PC 57169 MW; E463ABB40AC9FA82 CRC64;
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                                                                               27.3%; Score 1104; DB 1; 143.3%; Pred. No. 1.5e-69; cive 76; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSERKHQILSDVELKERSSKSLLANVLD
                                                                                                                                   Matches 227; Conservative
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                            498 AA;
                                                                                                            Similarity
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CARBOHYD
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                                                                                  Query Match
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Maldon D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Maldon D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,

RA Gebric B. Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Howland T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D.A., Howland T.J., Meil M.-H., Ibeywan C.,

RA Alalin D., Houston K.A., Howland T.J., Meil M.-H., Ibeywan C.,

Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalin D., Houston K.A., Howland T.J., Meil M.-H., Ibeywan C.,

Alalin W., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,

Mount S.M., Melson R.R., Mobarry C., Morris J., Moshrefi A.,

RA Malazolo M., Pittman G.S., Pan S., Pollard J., Moshrefi A.,

Ra Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V. Reese M.G.,

RA She B.C., Siden Kamong I., Simpson M., Strong R., Sun B.,

Ra Alazzolo M., Wooy M., Weinson M., Strong R., Sun E.,

RA Wang Z.Y., Wassarman D.A., Weinson D.K., Wang X.,

Wang Z.Y., Wassarman D.A., Weinsock G.M., Weissenbach J.,

RA Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: CNS in embryos.
-!- DEVELOPMENTAL STAGE: Late embryonic, late pupal and second instar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Biol. 3.RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: After binding acetylcholine, the AChR responds by extensive change in conformation that affects all subunits leads to opening of an ion-conducting channel across the pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS
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FlyBase; FBgn0000036; nAcR-alpha-96Aa. InterPro; IPR006629; New channel mer InterPro; IPR006202; New chan LED. InterPro; IPR006201; New channel.

; AE003747; AAF56301.2; -. S00381; ACFFA1.

EMBL; X07194; CAA30172.1;

Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                     243 YTVNLIIPCVGISFLSVLVPYLPSDSGEKISLCISILLSLTVFFLLABIIPPTSLTVPL
                                                                                                                                                                                                                                                                DVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                           ALPASHRFDLAAAGGISAHCFAEPPLPSSLPLPGADDDLFSPSGLNGDISPGCCPAAAAA
                                                                                                                                                                                                                                 SWIFLLIYLNES-AKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                           GTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL---
                                                                                                                                                                                                                                                                                                                               467 -QLQD----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLY
                                                                                                                                                                                                                                                                                                                                                              YFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                              -----WIRIVFLCWLPWILRMSRPGRPL
                                                                                                                                                                                                                                                                                                                                                                                                           303 LGKYLLFTWMLVTLSVVVTIAVLNVNFRSPVTHRMAPWVQRLFIQILFKLLCIERPKK--
                                                                                                                                                                                                                                                                                                                                                                                                                            ILEFPTTPCSDTSSERKHOILSDV-ELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLP
                      TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; WEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Polymorphism.
                                                                                                                                                                                                                  Gaps
                                                              PROTEIN, ALPHA
                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Y -> H.
                                                                                                                                                                                                                 Mismatches 168; Indels 102;
                                                                                                                                                                                                  Score 888; DB 1; Length
Pred. No. 2e-54;
                                                                                                                                                                           -> H (IN REF. 1).
08E1F721FB2A92AC CRC64;
                                                              ACETYLCHOLINE RECEPTOR
LIKE CHAIN 1.
EXTRACELLULAR.
                                                                                                                                                                   -> H.
-> H (IN REF.
                                                                                                                            SIMILARITY
                                                                                                             CYTOPLASMIC.
        Pfam; PF02932; Neur_chan_memb; 1
PRINTS; PR00252; NRTONCHANNEL.
                                                                                                                                                                                                                  91;
 Pfam; PF02931; Neur_chan_LBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 MFAILATIAVLLSAPHI 767
                                                                                                                                                                                   64019 MW;
                                                                                                                                                                                                   22.0%;
35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :: | :: | :: | 521 IACVVGTALIILQAPSL
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            664 HNPAFYR-----
                                                              567
                                                                              240
                                                                                                                                                                                  567 AA;
                                                                                                                                                                                                          Similarity
                                                                                                                                                   45
233
538
108
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241
272
3306
3326
149
222
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DISULFID
DISULFID
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                                                                             DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                   Query Match
                                                                                                                                                    CARBOHYD
                                                                                                                                                            CARBOHYD
                                                                                                     TRANSMEM
                                                                                                                                                                                                            Local
                                                                                                                                                                    VARIANT
                                                                                                              DOMAIN
                                                        SIGNAL
                                                                CHAIN
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516 AA

PRT;

STANDARD;

RESULT 8 ACH1 MANSE ID ACH1\_MANSE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 NQIMTINLWVEQSWYDYKLSWEPREYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                    Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 YLN---LSAKVCLAGYHEKRLIHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 NQLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; PS00236; NEUROTR ION CHANNEL; 1.
Transmembrane; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                     insect Manduca sexta.";

Eur. J. Neurosci. 10:879-889(1998).

-:- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
                  01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98424077; PubMed=97531155;
Bastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
"Characterization of a nicotinic acetylcholine receptor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E7A71E8C45D13BD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIKE CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.9%; Score 886; DB 1;
36.6%; Pred. No. 2.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, Y09795; CAA70928.1;
InterPro; IPR006029; Neu channel memb.
InterPro; IPR006020; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
Pfam; PF02931; Neur chan LBD; 1.
PFam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRTONCHANBL.
IIGREAMS; TIGR00866; LLC; I.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
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01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
28-FEB-2003 (Rel. 41,
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132
233
516 AA;
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                                                                                                                                                                                                  NCBI_TaxID=7130;
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                                                                                                                                                                                                                                                        307
                                                                                                                                                                                                                                                                                                    609
                                  128 KATLNYTGRVEWRPPALYKSSGEIDVEYFPFDQQTCVMKFGSWTYDGFQVDLRHIDEVRG 187
                                                                                                                                                                                                                                                                                                                                                   358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702
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                                                                                                                                                                                                                      610 TIPCSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGILPHNPAFY
    415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDBTGG
                                                                                                                                                                                             IIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
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                                                                                                  -----DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRTLYYFFNL
                                                                                                                                                                                                                                                                                               ---WIRIVFLCWLPWILRMSRPGRPLILEFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                                                    308 LFTMILDTFSICVTVVVLAVHFRSPQTHTMSPWVRRVFIHVLPRLLVMRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylolina receptor protein, alpha-Li chain precursor.
Schistocerca gregaria (Desert locust).
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PIR; S12359; S12359.
InterPro; IPR006029; Neu_channel_memb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 QTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL----QL 468
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                 JIUCERTO; IRNOVAZAI; NOUT CHAN IBD; 1.
Pfam; PF0231; Nour chan IBD; 1.
Pfam; PF0232; Nur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFĀMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 YLLFTMVLVGLSVVITIMVLNVHYRKPSTHKMAPWVRKVFIRRLPKLLLMRVPEQLL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 QLHHLQRPGGCNGLHSATNR--FG-GSAGAFGGLPSVVGLDGSLSDVATRKKYPFELEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 LKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAP 765
                                                                                                                                                                                                                                                                                        RECEPTOR ACTIVATION
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 557;
                                                                                                                                                                                                                                                                                                                                                                               168389C887DFDF3E CRC64;
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N-LINKED (GLCNAC.
ALA/SER-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                          21.6%; Score 873; DB 1;
36.8%; Pred. No. 2.2e-53;
ive 90; Mismatches 174;
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                                                                                                                                                                                                                                                                                                      SIMILARITY)
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                                                                                                                                                                                                                                            CYTOPLASMIC.
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                                                                                                                                      POTENTIAL.
IPR006202; Neur_chan_LBD_IPR006201; Neur_channel.
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                                                                                                                                                                                                                                                                                                                                                                             63026 MW;
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Q1582; Q9HAQ3;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Simi
Matches 197;
              InterPro;
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TRANSMEM
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TRANSMEM
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                                                                                                                                 SIGNAL
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ACH2 HUMAN
ID ACH2 HI
AC Q15822;
DT 01-NOV-
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MIN; 118502; ..., TAS., GO: 0005892; C: nicotinic acetylcholine-gated receptor-chan. ..; TAS., GO: 0005464; F: acetylcholine receptor activity; TAS., GO: 0010464; F: acetylcholine receptor activity; TAS., GO: 0010469; F: nicotinic acetylcholine-activated cation-se. ..; TAS., GO: 00007165; P: signal transduction; TAS., GO: 00007165; P: signal transduction; TAS., GO: 00007165; P: signal transduction; TAS., InterPro; IPR006029; Neur channel memb., TAS., InterPro; IPR006029; Neur channel.

R InterPro; IPR006029; Neur channel.

R Pfam; PF02931; Neur channel.

R Pfam; PF02932; Neur channel.

R Pfam; PF02932; Neur channel.

R Pfam; PF02932; Neur channel.

R Pfam; PF02925; Neur channel.

R PRINTS; PR00252; NEURONELANNEL.

R PRINTS; PR00252; NEURONELANNEL.

R PRINTS; PR00252; NEURONELANNEL.

R PRINTS; PR00252; NEURONEL ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBGNAT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blechschmidt K., Rosenthal A., Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                 TISSUE=Hypothalamus;
MEDLINE=97062879; PubMed=8906617;
Blliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson B.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA-2 CHAIN.
EXTRACELLULAR.
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC
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EMBL; X16X81; CAA76154.1; -.
EMBL; A7111103; -; NOT ANNOTATED_CDS.
Genew, HGNC:1956; CHRNĀ2.
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289
315
352
502
                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE FROM N.A
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265
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353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 VHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPPPPVEL---CHPLRLKLSPSYHWLESNV
                                                                                                                                                                                                        GSHTETEDRIFKHLFRGYNRWARPVPNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLK
                                                                                                                                                                                                                               366 LEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCL
                                                                                                                                                                                                                                                309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
                                                                                                                                                                                                                                                                                   YVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                            ------WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILSDV
                                                                                                                                                     75; Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH3 HUMAN STANDARD; PRT; 503 AA. p32297; Q15823; Q96RH3; Q99553; Q9BQ93; Q1-0CT-1993 (Rel. 27, Created) Q1-0CT-1993 (Rel. 35, Last sequence update) Q1-00CT-2003 (Rel. 42, Last annotation update) Meuronal acetylcholine receptor protein, alpha-3 chain precursor.
     BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                  (BY SIMILARITY).

**LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90245296; PubMed=2336208;
Fornasari D., Chini B., Tarroni P., Clementi F.;
"Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                          21.0%; Score 848.5; DB 1; Length 529; 36.7%; Pred. No. 1e-51;
                                                                                                                                       , Pred. No. 1e-51;
87; Mismatches 154; Indels
                                                                                      A -> T (IN REF. 3).
7F512B06CCD9AAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
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SEQUENCE FROM N.A. (ISOFORM 1).
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125
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129 1
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us-09-303-232-2.rsp

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A Strausberg R.L., Feingeld E.A., Grouse I.H., Derge J.G.,
A Klausner R.D. Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blata N.K.,
A Hopkins R.F., Jordan H., Moorer T., Mang J., Heish F.,
B Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
B Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McKennan F.J., McKernan K.J., Malek J.A., Gunzathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,
B Hahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=97162233; PubMed=9009220,

"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/Or IMR-32.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99118870; PubMed=9921897; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNB3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE=21342809; Pubmed=11450844;
MEDLINE=21342809; Pubmed=11450844;
Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.,
"Characterization of the human beta4 nAChR gene and polymorphisms in CHRNA3 and CHRNB4.";
                                                                    coding for the alpha 3 subunit
                                                                                                                                                               MEDLINE=97062879; PubMed=8906517;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson B.C., Velicelebi G., Harpold M.M.,
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
beta 4 subunits ",
J. Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Brain;
Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                        Mihovilovic M., Roses A.D.;
"Expression of mRNAs in human thymus coc of a neuronal acetylcholine receptor.";
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
                       MEDLINE=91114756; PubMed=1989896;
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TISSUE=Epidermal keratinocytes; Arredondo J., Grando S.A.; "Cloning cholinergic receptors in human keratinocytes.";

SEQUENCE OF 6-493 FROM N.A.

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MIM; 118503; -.

GO; GO: 00015464; F: acetylcholine-gated receptor-chan. .; TAS.
BR GO; GO: 00015464; F: acetylcholine activity; TAS.
BR GO; GO: 0001489; F: nicotinic acetylcholine-activated cation-se. .; TAS.
BR GO; GO: 0007165; F: transporter activity; TAS.
BR GO; GO: 0007165; F: transporter activity; TAS.
BR GO; GO: 0007165; F: transporter activity; TAS.
BR GO; GO: 0007165; F: transporter activity; TAS.
BR GO; GO: 0006810; F: transporter activity; TAS.
BR GO; GO: 0006810; F: transporter activity; TAS.
BR InterPro; IPR006203; Neu_chan. LBD.
BR InterPro; IPR006203; Neu_chan. LBD.
BR FFGAS; FR00252; Neur_chan. LBD.
BR FFGAS; FR00252; NRTCNCHĀNNEL.
TRANSPAMS; TIGR00860; LIC; N.
BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
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BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
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BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
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BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
BROSTIF; PS00236; NRCNCTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                  SUBUNIT: Neuronal AChR seems to be composed of two different type
Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                             IsoId=P32297-2; Sequence=VSP 000073;
Note=No experimental confirmation available;
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                     of subunits: alpha and non-alpha (betA).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                          IsoId=P32297-1; Sequence=Displayed;
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EMBL, AJ007784; CAR07682.1; --
EMBL, AJ007785; CAR07682.1; JOINED.
EMBL, AJ007785; CAR07682.1; JOINED.
EMBL, AJ007786; CAR07682.1; JOINED.
EMBL, BC001642; ARH01642.1; --
EMBL, BC002096; ARH02296.1; --
EMBL, BC000513; ARH05219.1; --
EMBL, RA385584; AAK68110.1; --
EMBL, X53559; CAR37625.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M86383; AAC84176.1; -.
EMBL, M37981; AAAS942.1; -.
EMBL, U62432; AA840110.1; -.
EMBL; Y08418; CAA69695.1; -.
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PIR; A53956; A53956.
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305
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                                                                                                                                                                                                     295 ILIYINLSAKVCLAGYHEKRLIHDILDPYNTLERPVINESDPLQLSFGLTLMQIIDVDEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FMTRPTSNEG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             618 SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGOGD 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 NAQKPRPLYGAELSNINCFSRAES------KGCKEGYPCQDGMCGYCHHRRIKISNF 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 678 DGSIGFIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFA 737
                                                                                                                                                                                                                             75
                                                                                                                                                                                                                    76 NQIMETNIWLKQIWNDYKLKWNPSDYGGABFWRVPAQKIWKPDIVLYNNAVGDFQVDDKT
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                                                                                                                                                                                                                                                    355 NOLLVINVWIKLEMNDMNIRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                        415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-50301489; PubMed-2114015;
Baumann A., Jonas P., Gundelfinger E.D.;
"Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
                                                                                                                                                                             64;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Accetylcholine receptor protein, alpha-like chain 2 precursor.
NACR-ALPHA-96AB OR ACRE OR SAD OR ACR96AB OR CG6844.
                                                 (IN REF.
6
                                                                                                                                                   Score 845; DB 1; Length 503;
Pred. No. 1.7e-51;
                                                                                                                                                                            97; Mismatches 166; Indels
(in isoform
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315 LSIVITVFVLNVHYRTPTHTMPSWVKTVFLNLLPRVM------
                                                                                                                         8A9EBC5D71AEC7D6 CRC64;
                                                VSLPLALSP -> ALAAPGAVA
LSPP -> CRA (IN REF. 1).
D -> G (IN REF. 1).
                                                                                                  -> S (IN REF. 1).
                                                                                     DD -> TT (IN REF.
            /FTId=VSP_000073.
                         L -> LL.
/FTId=VAR 013240.
MGSGPL
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                                                                                                                             57309 MW;
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Ruising-Reading acetyl-choline receptors;;

Nucleic factoring acetyl-choline receptors;;

Nucleic factoring acetyl-choline receptors;

Nucleic factoring acetyl-choline receptors;

Nucleic factoring acetyl-choline receptor protein of receptor factoring acetyl-choline receptor protein of receptors;

Nucleic factoring a movel alcocinic acetyl-choline receptor protein of receptors;

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gene: the ard gene of Drosc
FEBS Lett. 235:40-46(1988).
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the EMSLopean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 HSW-----IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPXNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DL----QLQD-----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 HIWRHCKPLCLLLVLLLLCETVQANPDAKRLYDDLLSNYNRLIRÞVSNNTDTVLVKLGLR 77
                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrame; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPAT
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                                                                                                                                                                                                                                                                                                                          ACETYLCHOLINE RECEPTOR PROTEIN, ALFHA-
LIKE CHAIN 2.
EXTRACELLULAR (POTENTIAL).
                       DEVELOPMENTAL STAGE: Late embryonic and late pupal stages. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
97D6A46CADC3F42F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 2.6e-51;
87; Mismatches 170; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 576;
    membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.9%; Score 843.5;
SUBCELLULAR LOCATION: Integral memb:
TISSUE SPECIFICITY: CNS in embryos.
DEVELOPMENTAL STAGE: Late embryonic
                                                                                                                                                                                                  InterPro; IPR006629; Neu channel memb-
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                           FlyBase; FBgn0000039; nAcR-alpha-96Ab
                                                                                                                                                                                                                                                                                                                PROBABLE.
                                                                                                                                                                                                                                    Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
PRIMTS; PR00252; NRIONCHÄNNEL.
TIGRFAMS; TIGR00860; LLC; 1.
                                                                                                                                                           AE003748; AAF56303.1; -. AY058446; AAL13675.1; -.
                                                                                                                                       EMBL; X52274; CAA36517.1; -.
EMBL; X53583; CAA37652.1; -.
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193; Conservative
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254
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Adams W.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Hichards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ruttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ra Ducbin K.J., Evangelista C.C., Ferriera S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                              410 MOMNSGGSSPDSLRRMOGRVGAGGCNGMHVTTATNRFSGLVGALGGGLSTLSGYNGLPSV 469
599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKE----RSSKSLLANVLDIDDDFRHNC 653
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                                                                                    ---KDLLRDLAANKINYGLKFSKTKFGOAL-MDB-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hermans-Borgmeyer I., Zopf D., Ryseck R.-P., Hovemann B., Betz H.,
Gundelfinger E.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Diptydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acctylcholine receptor protein, beta-like chain 1 precursor.
NACR-BETA-64B OR ACRD OR ARD OR ARD 61348/CG12606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of a developmentally regulated nicotinic
                                                                                                                                                                     --DGSIGPIGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetylcholine receptor protein from Drosophila.";
EMBO J. 5:1503-1508(1986).
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Mol. Cell. Biol. 8:778-785(1988).
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Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

A Harris N.L., Harwey D.A., Helman T.J., Hermandez J.R., Houck J.,

A Hostin D., Houston K.A., Helman T.J., Hermandez J.R., Houck J.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lux X., Mattei B. McIntosh T.C., McLood M.P., Mosherson D.,

Ra Lux X., Mattei B., McIntosh T.C., McLood M.P., Nosherefi A.,

Ra McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra McRon D.R., Nelson K., Nixon K., Nusny D.M., Nelson D.L.,

Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Ra Rahert K., Remingron K., Saunders R.D.C., Scheeler F., Shen H.,

Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

Syirskas R., Tector C., Turner R., Vehere E., Wang A.H., Wang X.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ra Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,

Ra Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;

Ra Turhe genome sequence of Incoophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flyasse; Fgron0000038; nAcR-beta-64B.
InterPro; IFR006029; Neur channel_memb.
InterPro; IFR006201; Neur chan LBD.
InterPro; IFR006201; Neur chan LBD.
From; PF02931; Neur chan memb; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
IIGRAMs; TIGR00860; LIC; I.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: CNS in embryos.
-!- DEVELOPMENTAL STAGE: Late embryonic and late pupal stages.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FF9BA2ABC0C3AA62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
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EMBL, X07956; CAA30778.1; --
EMBL, X07957; CAA30778.1; JOINED.
EMBL, X07958; CAA30778.1; JOINED.
EMBL, A20316; AAA28311.1; --
EMBL, AE003481; AAK47900.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Multigene family
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521 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 ------GLGD-----GCRRESESSDSILLSPEASKATE-----AVEFIAEHDRNE 462
                                                                                       665 NPARYRIVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTBYBLGLILKEIRFITDQLRKD
                                                                 291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQ11D
                                                                                                                                                                                                       411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQL-Q
                                                                                                                                                                                                                                                                                                  PCSDTSSERKHQILSDVELKERSS----KSLLANVLDIDDDFRHNC---RPMTPGGTLPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL--
                                                                                                                                      351 VDEKNQLLVTNVWLKLEWNDMNLRMNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                  ----DAVPLWIRIVFLCWLPWILRMSRPGRPLILEFPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-88283624; PubMed=3267226;
Nef P., Omeyser C., Alliod C., Couturier S., Ballivet M.;
"Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
EMBO J. 7:595-601(1988).
-:- FUNCTION. After binding acetylcholine, the AChR responds by an
extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1980 (Rel. 11, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (also called beta). A functional receptor seems to consist of two alpha-chains and three non-alpha chains. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                70;
20.8%; Score 840; DB 1; Length 521; 35.6%; Pred. No. 3.9e-51;
                                                                                                                                                                                                                                                                                                                                               PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 AA
                                  95; Mismatches
   Query Match 20.8°
Best Local Similarity 35.6°
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEKNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 TGGDISSYVLNGEWELLGVPGKRNELYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCV 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||: : :| | | | | | ||::| :::|||||||| :: | :|:|| :||
LISCLTVLVFYLPSDCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 FVTLSIIITVFVLAVHHRSPSTHTMPHWVRSFFLGFIPRWLFWKRP--PLLLPAEGTTGQ 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WCFVTLQAATREQKQPHGFAEDRLFKHLFTGYNRWSRPVPNTSDVVIVKFGLSIAQLIDV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EFPTTPC----SDTSSERKHQILSDVELKERSSKSLLANVL---DIDDDFRHN 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 HHVDLKDYWESGEWAIINAIGRYNSKKYDCCTEIYPDITFYFVIRKLPLFYTINLIIPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                              NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----WIRIVFLCWLPWILRMSRPGRPLIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
POSTSYDAPLIC membrane; Ionic Channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E76C6360AF876364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                         EMBL; X07339; CAB55645.1; -...
EMBL; X07340; CAB59645.1; -...
EMBL; X07341; CAB59645.1; JOINED.
EMBL; X07342; CAB59645.1; JOINED.
EMBL; X07343; CAB59645.1; JOINED.
EMBL; X07343; CAB59645.1; JOINED.
EMBL; X07344; CAB59645.1; JOINED.
EMBL; AJ250360; CAB59645.1; JOINED.
EMBL; AJ250360; CAB59625.1; -..
PIR; S00377; ACCH2N.
InterPro; IPR006029; Neur_chan.ell.
InterPro; IPR006201; Neur_chan.lbD.
InterPro; IPR006201; Neur_chan.lbD.
Ffam; PF02931; Neur_chan_lbD; I.
PFIAM; PF02931; Neur_chan_lbD; I.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Multigene family.
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528 AA;
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394
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DISULFID
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TRANSMEM
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371 YDPPGTRLSTSRCWLETDVDDKWEEEEEEEEEEEEEEEEKAYPSRVPSGGSQGTQCHYS 430
                                              709
                                                                                  467
                                        CRPM---TPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGL
                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Pentamer of two alpha chains, and one each of the beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P., "A 5'-flanking region of the chicken acetylcholine receptor alphasubunit gene confers tissue specificity and developmental control expression in transfected cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  delta, and gamma chains.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                        710 ILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTWFAILATIAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-84206570; PubMed-6327170;
Ballivet M., Nef P., Stalder R., Fulpius B.;
"Genomic sequences encoding the alpha-subunit of acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M., "Genes expressed in the brain define three distinct neuronal micotinic acetylcholine receptors.";
EMBO J. 7:595-601(1988).
                                                                              431 CERQAGKASGGPAPQVPLKGEEV---GSDQ-----GLTLSPSILR-
                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cold Spring Harb. Symp. Quant. Biol. 48:83~87(1983)
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N-LINKED (GLCNAC. . .) (PROBABLE).

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Search completed: May 7, 2004, 11:36:31 Job time : 16.3803 secs Н

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GenCore version 5.1.6
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using sw model protein search, OM protein -

7, 2004, 11:30:03 ; Search time 48.3701 Seconds (without alignments) 5022.709 Million cell updates/sec Мау Run on:

US-09-303-232-2 Title: Perfect score:

4043 1 MKNAQLKLTEVDDDELWLAV.....MFAILATIAVLLSAPHIIVS BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1017041 segs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:\* Database :

sp\_archa:\*
sp\_bacteria:\*
sp\_tungi:\*
sp\_tungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\* unclassified: \* vertebrate:\* sp\_bacteriap:\* sp\_rodent:\* rvirus:\* archeap: sp plant:\* virus:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

heliothis v 28t7v5 drosophila drosophila drosophila drosophila drosophila drosophila Description 09vjt9 08t5f5 086mn7 096mn7 09xzi3 08t7s2 08t7s3 08t7s3 08t7s3 08t7s9 Q9VWI9 Q9XZI3 Q8T7S2 Q8T7S3 Q8T7S1 Q8T7S1 Q8T7R9 Q8T7R9 Q9XZI4 Q8T7R9 Q9YZI4 Q9VJT9 Q8T5F5 Q86MN7 Q8T7V5 Query Match Length DB 545 4494 4944 4944 5233 501 49.2 45.8 40.2 40.1 2613 2388.5 1991 1988 1625.5 1622.5 1621.5 1620.5 Score No. Result

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### ALIGNMENTS

SEQUENCE FROM N.A.
MEDLINE=21969411; PubMed=11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Grauso M., Renoinic Acetylcholine Receptor Subunit Genes,
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalphar, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNAMediated A-to-I Pre-mRNA Editing.", 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
CG449B OR CG1687B OR CG12975.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Buydroidea; Drosophilidae; Diptera; Brachycera; Muscomorpha;
NOBI\_TAXID=7227; 807 AA PRT; PRELIMINARY; Q8T7V5 RESULT 1 DTT DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DDT T DD

. .; IEA. Genetics 160:1519-1533(D202).
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
-- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
--- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
--- FLYBRAGE; FEBONO28875; DACR-alpha-34E.
--- GO; GO:0005201; F:extracellular ligand-gated ion channel activ...;
--- GO; GO:0005216; F:ion channel activity; IEA.
--- GO; GO:0005216; F:ion channel activity; IEA.
--- GO; GO:0005218; F:symaptic transmission; IEA.
--- GO; GO:0005218; P:symaptic transmission; IEA. InterPro; IPR006201; Neur\_channel.
InterPro; IPR006202; Neur\_chan LBD.
InterPro; IPR006029; Neur\_chan LBD.
InterPro; IPR006029; Neur\_chan LBD.
Pfam; PF02931; Neur\_chan LBD; 1.
Pfam; PF02932; Neur\_chan memb; 1.

heliothis v drosophila

440.1 339.8 339.6 32.7 30.7 30.5

1609

drosophila drosophila drosophila

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FlyBase
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             TIGRPAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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                                                                             91223 MW;
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Best Local Similarity 95.4'
                                                                           807 AA;
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PRT;

O9VJT9; 01-MAY-2000 (TrEMBLrel. 13, Created)

PRELIMINARY;

QPUJT9

RESULT 2 Q9VJT9

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REM PLDINES-12196006; PubMed=10731132;

Adams M.D. Celniker S.E. Li P.W. Hoskins R.A., Gocayne J.D.,

Adams M.D., Celniker S.E. Li P.W. Hoskins R.A., Galle R.F.,

RA George R.A. Lewis S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Barndon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Barndon R.C., Rogers Y.H., Blazej R.G., Change M., Pfelffer B.D.,

RA Ballew R.M., Basu A., Barachala J. Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Cawles B.D. Bouck J., Broketein D., Brottler P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Burtis K.C., Busam D.A., Bouck J., Brokenport L.B., Davites P.,

RA Burtis K.C., Busam D.A., Boung Z., Mays A.D., Dew I., Dietz S.M.,

RA Posler C., Gabrialian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Gong F., Gorrell J.H., G. Z., Gan P., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Melman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D., Melman T.J., Merandez J.R., Houck J.,

RA Harris N.L., Marvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Laix N., Mattei B., McIncoh T.C., Morison M.P., Morlson D.L.,

RA Martis M. Woy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

RA Balazon D.R., Nelson K.A., Bwanger R.D., Pollard J., Wang S.,

RA Balazon M., Pittman G.S., Pan S., Pollard J., Wang S., Yao Q.A., Ye J.,

RA Balazon D.R., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Reinert K., Remington K., Stunders R., Wenter E., Shen H.,

RA Reinert K., Remington K., Stunders R., Wenter E., Shen H.,

RA Rheng X.H., Zhong W., Rubiscock G.M., Weissenbach H.,

RA Sheng X.H., Zhong W., Rubiscock G.M., Weissenbach H.,

RA R
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EMBL, ARE03462; AFFS3374-3; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
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                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroidea, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
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NACRALPHA-34E OR CG32975.
(TrEMBLrel.
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                                                                                                                                                                                                            TTQQPINIRLCARKRQRLRRRRRKRXPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----W--FSVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLIASMALL 469
                                                                                                                                                                                                                                                                                                                                                                                     ---DEKNÖLLV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         629
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                                                                                                                                                                        MENAQLKLTEVDDDBLWLAVRLAHCSSNISSSSTRTTSSNKRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                                                              TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
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                                                                                                                                                       1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 WLKKDDECNDIANDWKFAAMVVDRLCLIFTMFTILATIAVLLSAPHIVS
GO; GO:0030594; F:neurocramsport; IEA.

GO; GO:0006811; P:ion transport; IEA.

R InterPro; IPR006201; Neur channel.

R InterPro; IPR006202; Neu channel memb.

R Pfam; PF02931; Neur chan LBD.

R Pfam; PF02932; Neur chan LBD.

R Pfam; PF02932; Neur chan LBD.

R PRIMTS; RR00252; NEUROTRANNEL; 1.

SRQUENCE 570 AA; 64767 MW; DBB21E1E185263BF CRC64;
      receptor activity; IEA
                                                                                                                                     20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQV---
                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 GFTLPPDSGEKLSLGT----YFNCIMFMVASSVVSTI---
                                                                                                               64.6%; Score 2613; DB 5; 69.0%; Pred. No. 1e-219;
                                                                                                                                  17; Mismatches
                                                                                                         Query Match
Best Local Similarity 69.09
Matches 532; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LILINY-
                                                                                                                                                                                                                                                                                                                                                                                                      360
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AC QBTS
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AA. 482

Created) PRT;

O8T5F5; 01-JUN-2002 (TrEMBLrel. 21,

PRELIMINARY;

Q8T5F5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                       A SACURAL FACUR. N. A. M. S. MEDLINE-2196941; PubMed=11973307; A MEDLINE-2196941; PubMed=11973307; A Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; The Second M. Reenan R.A., Culetto E., Sattelle D.B.; The Second M. Seenan R.A., Culetto E., Sattelle D.B.; The Modiated A-to-1 Pre-mRNA Editing.", Adenosine Deaminase Acting on RNA-ST Genetics 160:1519-1533(2002).

C. -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

DR FUBBL, AAV036613, AAK67256.1; -.

DR GO: GO:0005210; F: extracellular ligand-gated ion channel acti. . .; IEA

GO: GO:0005210; F: extracellular ligand-gated ion channel acti. . .; IEA

GO: GO:0006210; P: transmission; IEA.

DR GO: 00005210; P: transmission; IEA.

DR GO: 00005210; P: transmission; IEA.

DR GO: 00005210; Neur-chan LBD.

BR InterPro; IPR006201; Neur-chan LBD.

BR PRINTS; PR00525; NEURONCHĀNNEL. 1.

DR PRINTS; PR00525; NEURONCHĀNNEL. 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalphas subunit.
NACR-ALPHA-34E OR NACRALPHA34E OR BG:DS05899.4 OR BG:DS05899.5
CG4498 OR CG16678 OR CG32975.
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H
                                                                                                                                                                                              Insecta; Pterygota;
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.3
Matches 457; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 AA;
                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPÇV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 AGGDISSFITWGEWDLLGVPGKRNEIYYNCCPEPYIDITFALLIRRKTLYYFFULIVPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCS
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NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLIY---LNESAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
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                                                                                                                                                                                                                                                                                                                                  Millar N.S.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ554210; CAD86536.1; -.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:003230; F:extracellular ligand-gated ion channel acti...;

R GO; GO:003524; F:neurotransmitter receptor activity; IEA.

R GO; GO:0006811; P:ion transport; IEA.

R InterPro; IPR006520; Neur channel.

R InterPro; IPR006520; Neur channel.

R Pfam; PF02931; Neur chan LBD;

R Pfam; PF02931; Neur chan LBD; 1.

R Pfam; PF02932; Neur chan LBD; 1.

R RINTS; PR00552; NRIONCHĀNNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNWVAETMPATSDAVPL
                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.2%; Score 1991; DB 5; Length 54; 72.8%; Pred. No. 2.7e-165; ive 43; Mismatches 46; Indels
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                                           542 AA.
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PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
                                           PRT;
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                                             PRELIMINARY;
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542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Receptor.
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Matches 382;
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RAMEDINE=2019 8006; PubMed=10/3112;
RAMEDINE=2019 8006; PubMed=10/3112;
RAMEDINE=2019 8006; PubMed=10/3112;
RAMEDINE=2019 8006; PubMed=10/3112;
RAMEDINE=2019 8006; PubMed=10/3112;
RAMEDINE=2019 8006; PubMed=10/312;
RAMEDIO G.G., Rochers S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RAMEDIO G.G., Worthan J.R., Palazej R.G., Chango M., Miklos G.L.G.,
RAMEDIO G.G., Rochers E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RAMEDIO F.C., Bayer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RAMEDIO F.C., Bayernal B.P., Bhandari D., Basaley E.M.,
RAMEDIO F.C., Burnan B.P., Bhandari D., Beasley E.M.,
RAMEDIO F.C., Burnan B.P., Bhandari D., Bolahakov S.,
RAMEDIO F.C., Burler H., Cadleu B., Center A., Charler P.,
RAMEDIO F.C., Burler H., Cadleu B., Center A., Chun P.,
RAMEDIO F.C., Burler A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RAMEDIO K.J., Evangelista C.C., Perraz C., Ferriara S., Paleischmann W.,
RAMEDIO K.J., Evangelista C.C., Perraz C., Ferriara S., Paleischmann M.,
RAMEDIO K.J., Harvey D., Hehman T.J., Herrinadez J.R., Harris M.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
Alali M., Marthin A.M., Nixon K., Nusskern D.L.,
RAMEDO B., Mishina N.W., Wortneed M.P., Moshrefi A.,
Reson R.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ramed B.E., Spradling A.C., Stapleton M., Strong R., Shen H.,
Ryinkas R., Tector C., Turner R., Vence B., Shen H.,
Ryinkas R., Merch G.M., Walssenbach J.,
Ryinkas R., Merch E., Wassarman D.A., Wellsenbach J.,
Williams S.M., Woodsey T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
Ryinkas R., Mang Z.-Y., Wassarman D.A., Wellsenbach S., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu X., Zhu 
435 MYRQGDDGSVGPVGPAGPVVDGRLHEAIS-HTCLTSSAEYELALILKELRWITEQLKKED 493
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Ranarides P.G., Brandon R.C., Rogers Y.,

Evans C.A., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG32538 protein.
NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
Drosophia melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopeera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                           726 ECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              545 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q9VWI9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNSSEFGGVRDLRIPPHRLWK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDVLMYNSADEGFDGTYAINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                            Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Photanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                        , Pred. No. 4.9e-165; Length 545; 46; Mismatches 51.
                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0031014; nAck-alpha-18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.2%;
71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; IEA.
                                                                                                                          710 ILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFALLATIAVLLSAPHIIV
556 MTPGGTLPHNPAFYRTVYGQGDDGSIGPIGST-----RMPDAVTHHTCIKSSTEYELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea,
Noctuidae, Heliothinae, Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVINESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LILLCLIMPRGARCGYHEKRLIHHLLDHYNVLERPVVNESDPLOLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
butative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.8%; Score 1850; DB 5;
70.0%; Pred. No. 5.1e-153;
iive 30; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                     496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                     S 541
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256
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CHECKLOLIAR LOCATION: THE LIGAND-GATED IONIC CHANNEL FAMILY.

BY LYBASE; FEBRONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

EMBL; AF31446, AAM13393.1;

BY LYBASE; FEBRONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

BY CO. GO: 0016221; AAM13393.1;

CO. GO: 0016221; C: integral to membrane; IEA.

GO: GO: 0005230; F: extracellular ligand-gated ion channel acti. . .; IEA.

GO: GO: 0005216; F: ion channel activity; IEA.

GO: GO: 0005216; F: ion channel activity; IEA.

GO: GO: 0005216; F: ion channel activity; IEA.

GO: GO: 0005216; F: ion channel activity; IEA.

GO: GO: 0005201; Neur-channel.

INTERPRO; IPRO06202; Neur-channel.

R THERPO; IPRO06202; Neur-channel.

R Ffam; PF02391; Neur-channel.

R Ffam; PF02392; Neur-channel.

R FINT; PRO0525; NEURONEANNEL.

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DISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA
                                                                                                                                                                                                                                                                               -----LAAHSCF--GVDYELSLILKEIRVITDQMRKDDEDADISRDW
                                                         -WIRIVFLCWLPWILRMSRPG---RPLILEFPTTPCS
                                                                                                                                                                          DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                QGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW
                                                                                                                                       317 SSVVSTILILNYHHRHADTHEMSDWİRCVFLYWLEWVLRMSREGSATTEPPPARVEPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21969411; PubMed=11973307;
Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533(2002).
                                                                                                                                                                                                             -----PQAQOPQCCRYYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (II).
Bukaryota, Metazoa, Arhropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                    770
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                                                                                                                                                                                                                                                                                                                   KFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIVS
                                                                                                                                                                                                                                                                                                                                     494 AA
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61.4%;
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Best Local
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                                                                                                                                                                                                                                                         TYQINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470
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                                         68
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10 SLFVLLIFLAIIKESC-QGPHEKRLIAHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                                                                                                           69 VDEKNQLLITULMLSLEMNDYNLRMNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAESMPTTSDAVPLIGTYFNCIM
                                                                                                                 VDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLR I PPHR I WKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                             129 TYHTNIVVKHGGSCLYVPPGIFKSTCKMDIIWFPFDDQHCEMKFGSWTYDGNQLDLVLNS
                                                                                                                                                                                                                                                                                                                                                                                                         ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNLIIPC
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MEDINE-21969411; PubMed=11973307;

MEDINE-21969411; PubMed=11973307;

Grauso M., Reeman R.A., Culetto E., Sattelle D.B.;

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533 (2002).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amotation update)
Nicotinic accetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLQWLPWİLRMGRPGRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
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G0:0005230; F:extracellular ligand-gated ion channel a
G0:0005216; F:ion channel activity; IEA.
G0:0030594; F:neurortransmitter receptor activity; IEA.
G0:0006811; P:ion transport; IEA.
G0:0007268; P:synaptic transmission; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI----
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006202; Neur_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
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FlyBase; FBgn0032151; nAcR-alpha-30D.
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320; Conservative

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Similarity

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                                                                                                                                                                                                                                                        291 SWIFLLIYLNASAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMOIID
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Millar N.S.;
Mullar N.S.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ554209; CAD86535.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti...
GO; GO:0005611; F:ion transport; IEA.
InterPro; IPR006201; Neur_channel.
                                                                                                                                                                                                                   79;
                                                                                                                                                                            494;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                       Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 FMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLOWLPWILRMGRPGRKI
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha6 precursor.
NACRALPHA-30D.
                                                                                                                                                                            Length
                                                                                                                                                                                                                 77; Indels
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                                                                                                                                                                        ; Score 1622.5; DB 5;
; Pred. No. 4.1e-133;
46; Mismatches 77;
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Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
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Matches 319; Conservative
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                                                                                                                                                                                                POTENTIAL. NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                   291 SWIFLLIYLNESAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMOIID
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                                                                                                                                                                                                                                                                                                                                                                     16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLOWLPWİLRMGRPGRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLIASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG4128
                                                                                                                                                                                                                                                                                                                       DB 5; Length
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotinic acetylcholine receptor Dalpha6 subunit variant
                                                                                                                                                                                                                                                                       4DFC572139587070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 DIANDWKFAAMVVDRLCLIIFIMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## 453 ELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV
                                                                                                                                                                                                                                                                                              40.1%; Score 1621.5; DB 5; 61.4%; Pred. No. 5.1e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ď.
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InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006029; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIOWCHANDEL.
IIGRAMS; TIGR0860; LIC; 1.
                                                                                                                                                                                                                                              DALPHA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21969411; PubMed=11973307;
                                                                                                                                                                                                                                                                       494 AA; 55980 MW;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                26
494
                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                       Signal; Receptor SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Best Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYHTNIVVÆHSGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 VLISSMALLGFTLPPDSGEKLTLGVTILLSLIVFLNLVAETLPQVSDAIPLLGTYFNCIM 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SGSQTAIGSSASFGRPTTVEEHHTAI-GCNHKDLHLILKELQFITARNRKADDBA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                  .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                             351 VDEKNOLLVINVMLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               670 RTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKEIRFITDQLRKDDECN
                                                                                                                                                                                                                                                                                                                                                                                                              SWIFLLIYLNESAKVCLAGYHEKRLIHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
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            Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Baliting."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLQWLPWİLRMGRPGRKI-----
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                              -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321447; AAM13394.1; -.
                                                                                            Figure 1 Property 1 August 1954.1, 1.

FyBase, FBgn0032151; nAck-alpha-30D.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005216; F:extracellular ligand-gated ion channel acti...

GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:000526; F:ion transport; IEA.

GO; GO:0007268; P:synaptic transmission; IEA.

InterPro; IPR006201; Neur_channel.

InterPro; IPR006201; Neur_channel.

InterPro; IPR006029; Neur_chanleD.

Fam; PF02931; Neur_chanleD.

Fam; PF02931; Neur_chan memb, 1.
                                                                                                                                                                                                                                                                                                                                                                                     79;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
                                                                                                                                                                                                                                                                                                                                                            5; Length 494;
                                                                                                                                                                                                                                                                                                        Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                      75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELIGDWKFAAMVVDRFCLIVFTLFTIATVTVLLSAPHIIV 493
                                                                                                                                                                                                                                                                                                                                 494 AA; 56113 MW; 48327537229573FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.2e-133;
9; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                           40.1%; Score 1620.5;
                                                                                                                                                                                                                                                                                          PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                   Pfam; PF02932; Neur chan memb; 1. PRINTS; PR00252; NRIONCHĀNNEL.
                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.0%;
Matches 318; Conservative 4
                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0860; LIC; 1
                                                                                                                                                                                                                                                                                                                   Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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523 AA.

01-JUN-2002 (TrEMBLrel. 21, Created)

Q8T7R9; Q8T7R9

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VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAESMPTTSDAVPLIGVTILLSL 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDEKNQILTTNAMINLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 TVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPPWIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 NVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCI
                                                                                                                                                                                                                                                                                                                                          SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFVLLIFLAIIKESC-QGPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TRKTILLSNRMKELELKERSSKSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .
GO; GO:0005216; F:enchannel activity; IEA.
GO; GO:000524; F:enchannel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR006202; Neur channel.
InterPro; IPR006202; Neur channel.
InterPro; IPR006202; Neur channel.
Ffam; PF02931; Neur channel.
Pfam; PF02931; Neur channel.
Pfam; PF02931; Neur channel.
Pfam; PF02931; Neur chan memb.
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinia cacetyclocilne receptor Dalphas subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Evkaryorta, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C200AF74F87F841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 4.6e-132; 46; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch
39.8%; Score 1611;
al Similarity 58.2%; Pred. No. 4.4
320; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVFLOWLPWILRMGRPGRKI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0860; LIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; NEUROTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 AA;
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617

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Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Myorel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,

Thowel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,

The Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-

The Mediated A-to-I Fre-mRNA Editing.";

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

Genetics 160:1519-1533 (2002).

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Genetics 160:1519-1533 (2
                                                                                                                      SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMNTR
                                                                                              -WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                                                                              SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                                                                                                                                                                                 YGOG-----DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACR-HENA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 509;
                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                      DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
        SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.6%; Score 1602; DB 5;
59.3%; Pred. No. 2.7e-131;
iive 48; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 AA.
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006029; Neu channel memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02931; Neur chan LBD; 1. Pfam; PF02932; Neur chan memb; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO0860; LIC;
PROSITE; PS00236; NEUROTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 59.3
Matches 318; Conservative
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SEQUENCE 1
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  KSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIA 759
                                                                                       414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte T., Oellers N., Adamczewski M.;

"Futative alpha subunits of insect nicotinic acetylcholine receptors
T "Futative alpha subunits of insect nicotinic acetylcholine receptor alpha subunits of insect nicotinic acetylcholine receptor alpha subunits.";

T to other insect nicotinic acetylcholine receptor alpha subunits.";

L Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
-: SUBCELLULAR LYCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

R EMBL, AR143847; AAD32698.1; --
R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015216; F:ion channel activity; IEA.

GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005811; P:ion transport; IEA.

GO; GO:0007268; P:synaptic transmission; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . . : IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Heliothis virescens (Noctuid moth) (Owlet moth).
Bukaryota, Matazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota, Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae, Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLALIPVSEQ----GPHEKRLINALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501;
                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.8%; Score 1609; DB 5; 60.8%; Pred. No. 6.4e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                         501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan LBD.
InterPro; IPR006029; Neu_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00252; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0860; LIC; 1
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                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                      769
                                                                                                                                                                                              522
VLLSAPHIIV
                                                                                                                                                                                         513 VLLSAPHIIV
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sst Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7102;
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                                                                200
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                                                                                                                                                      091
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                                                                                                                                                                                                                                                                                                     Q9XZI4
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Gaps

94;

68

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575
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                                                                                                                                                                                                                                                                                                                                                                                                         413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452
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"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                      RRRTLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPAT
                                                                                                                                                                                                                                         249 RRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLLPQV
                                                                                                                                                                                                                                                                                                                                                                                            ---TRKIILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI
 -DEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWK
                     69 VDEKNQILTTNAMINLDEKNQLLITNIMLSLEWNDYNLRWNETEYGGVKDLRITPNKLWK
                                                                                          SWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII
                                                                                                                                                                                                                                                                                                                                309 SDAIPLLGTYFNCIMFMVASSVVLTVVVLNXHHRTADIHEMPPWIKSVFLOWLPWILRMG
                                                                                                                                                                                                                                                                                                                                                                    599 RPGRPLILEFPTTPCSDTSSERKHQILS----DVELKERSSKSLLANVLDIDDDFRHNCR
                                                                       PDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG
                                                                                                                                                                    189 SWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYACCPEPYVDITFTIQI
                                                                                                                                                                                                                                                                                                 ----WIRIVFLCWLPWILRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                              655 PMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SGSQTAIGSSASFGRPTTVEEHHTAI-GCNHKDLHLILKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       714 IRFITDQLRKDDECNDİANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Hewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
NACR-ALPHA-34E OR BG:DS05899,4 OR BG:DS05899.5 OR CG4498 OR CG16878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR CG32975.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Muscomorpha; Ephydroidea; Drosophilae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                               SDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         369 RPGRKI-
                                                                                                                                              456
                                                                                                                                                                                                                        516
                                                                       396
351
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celliker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
A Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Mar K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Boslek S. M.,
Berneson K.W., Bennes P.P., Bhandari D., Boslek S. M.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Berlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Carley J.M., Carley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup D.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Carley G.M., Goorg F., Gerraz C., Ferriaca S., Pleischmann W.,
R. Borten D., Hourey D., Heiman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harrey D., Heiman T.J., Wein M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha; Ephydroidea, Drosophilae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                5; Length 391;
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                                                                                                     E2AB465CF275E8C0 CRC64;
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Pred. No. 1e-122;
5; Mismatches 11
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FlyBase, regn0028875; nAcR-alpha-34E. Hypochetical protein. SEQUENCE 391 AA; 43974 MW: F?PRAF!
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MEDLINE=20196006; PubMed=10731132;
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94.4%;
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RMEL, ABOUSACS, AAFS28H7.2 -...
RRIL, ABOUSACS, AAFS28H7.2 -...
R PlyBase; FEGNO032151; nAcR-alpha-30D.
R OG, 6000520; Cimembrane; TEA.
GO; 60005230; F:extracellular lEA.
GO; GO:0005230; F:extracellular lEA.
GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
RO; GO:0030594; F:neurotransmitter receptor activity; IEA.
InterPro; IPR006202; Neur_chanell.
RILEPPO; IPR006202; Neur_chanell.
RILEPPO; IPR006202; Neur_chanell.
REAM: PF02931; Neur_chan_LBD; 1.
REAM: PF02931; Neur_chan_memb; 1.
REAM: PF02932; Neur_chan_memb; 1.
RIGRAMS; TGCR00860; LIC; ILC; ILC;
RRICHANS; TGCR00860; LIC; ILC;
RROSITE; PS00236; NeUROTR ION CHANNEL; 1.
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Bulu X., Martei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy E., Murphy L., Muzry D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J., Milliams S.M., Woodage T., Weinstock G.M., Wissenbach J., Ke J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Barson J., An H., Baldwin D., Baranon R.C., Rogers Y.,

Barson J., An H., Baldwin D., Barson J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Gorden K., Dorsett V., Hostins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,

Rapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., mogall C.J., Lewis S.E.,
"Annotation of Drosophia melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID 350
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                                                                                         69 VDEKNOLLITULMLSLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                   10 SLFVLLIFLAIIKESC-QGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                      351 VDEKNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
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Search completed: May 7, 2004, 11:38:36 52.3701 secs Job time :

15;

Gaps

Best Local Similarity 47.99 Matches 286; Conservative

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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- nucleic search, using frame\_plus\_p2n model OM protein

May Run on:

8, 2004, 11:50:34 ; Search time 5376.49 Seconds (without alignments) 4276.744 Million cell updates/sec

US-09-303-232-2

4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAFHIIVS 770 score: Sequence: Title: Perfect

Xgapon 10.0, Xgapext Ygapon 10.0, Ygapext Ygapon 10.0, Ygapext Fgapon 6.0, Fgapext Delop 6.0, Delext **BLOSUM62** Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

length: 20000000000 length: 0 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/Cogn2\_1/USPTO spool/1/US030323.Z/runat\_07052004\_101110\_23893/app\_query.fasta\_1.2261
-Q=/Cogn2\_1/USPTO spool/1/US030323.Z/runat\_07052004\_101110\_23893/app\_query.fasta\_1.2261
-DB=EST\_QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 +BAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0930323\_@CGN\_1 1 4577 @runat\_07052004\_101110\_23893 -NCPU=6 -ICPU=3
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

gb\_est4:\*
gb\_est5:\*
em\_estfun:\*
em\_estfun:\* em\_estba:\*
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em\_estcov:\* em\_estpl:, em\_estro:, em\_htc:\*, gb\_estl:\* gb\_htc:\*, gb\_est2:\* EST:\*

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* vrt:\* em gss 

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em gss fun:\*

gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

cription	632919 GH	530299 4	57 AGENCO	873	1497 Mils m	1730	Mus	Mus	Homc	AY406230 Homo sapi	Mus m		Mus	Pan	Mus	Mus	Mus	9013	9722 Mus	2	BU149265 AGENCOURT	4 Mus	31 Pan	_	4	211	BM639954 170006876	0	μ:	4 .	a .	00 901346	2 901346	OF CHOICE	Muse and was	1 Droeonh	186 Mile mile	771 Mile mil	506 BY72	19460 W-FST03	45337 III M. DVO	739825 TIT-M-DD	087554 Mus m
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### ALIGNMENTS

EST 23-APR-2001

BG632919

GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919.1 GI:13758409 EST. BG632919 RESULT 1 BG632919/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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542

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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r. For more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CH03QPI&cluster=7646.r. Contact :
Feng Liang Email : fliang@lifetech.com URL:
Feng Liang Email : fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CH03QPI.
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1 (bases 1 to 1201)

1 (bases 1 to 1201)

1 (hases 1 to 1201)

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12793792.
                                                                                                                                                                                                                                                                                                                                                                                                                                     563 ValpheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAlaValProLeu 581
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                                                                                                                                      PhePheAsnLeullelleProCysValLeulleAlaSerMetAlaLeuLeuGlyPheThr
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                         ProGluProTyr11eAsp11eThrPheAla11e11e11eArgArgArgThrLeuTyrTyr
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/mol_type="mRNA"
/db xref="taxon:727"
/dlone="GH16126"
/sex="male and female"
/sex="male and female"
/dev stage="adult"
/lab_bost="DH5 - alpha"
/clone lib="GH brosophila melanogaster head pOT2"
/note="lorgan: head; Vector: pOT2; Site 1: ECOR1; Site 2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
                                                                                                                                                                                                                                             Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 East. 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AB00351: arm:X [18792641,19136447] estimated-cyto:18A3-18Gs: 04110/2001 Plate: GH.161 row. C column: 2 Plate: GH.191 sequence stopp: 784.
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BDGP/HHMI Drosophila EST Project
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                                                                                                                                                  Unpublished (2001)
Other ESTs: GH16126.5prime
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/note="Vector: pcMv-SPORT6; Site_1: Not1; Site_2: Sal1;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219
                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can !
http://image.llnl.gov
Plate: LLAMA4238 row: f column: 14
High quality sequence stop: 746.
Location/Qualifiers
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      1 (bases 1 to 922)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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158
50
43
26
                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="IMAGE:6642638"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                          organism="Xenopus laevis"
                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                    GCAAGCGAGTWCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTGGAG 246
                                                              ArgProValLeuAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGln 347
                                                                                   IlelleAspValAspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGlu 367
                                                                                                                                                   388 IleProProHisArgileTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGly 407
                                                                                                                                                                                                                                                                                                                                 PheAspGlyThrTyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrVal 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnArgCysGluMetLysPheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGln 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlnAspGluThrGlyGlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeu 487
AlaGlyTyrHisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGlu 327
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                               TrpAsnAspMetAsnLeuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GlyGluLysLeuSerLeu-GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etValAlaGluThrMetProAlaThrSerAspAlaValProLeuTrplleArg----
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BU915857.1 GI:24097771
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ACCESSION VERSION KEYWORDS

RESULT 3 BU915857

629 GluLeuLysGluArgSerSerLysSerLeuLeuAl. ::: :::       1400 GATGCCGAGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGG	δδ.	OS-09-303-232-2 (1-770) X CD013901 (1-2296)  QY 309 GlyTyrHisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThr 325	
609 ProThrThrProCysSerAspThrSerSerGluAry	S da	20.99% Indels: 14 Gaps:	
589 CysTrpLeuDroTrplleLeuArgMetSerArgPr 	ò q	Alignment SCOIDS: 4.25e-65 Length: 2296  Pred. No.: 848.50 Matches: 183  Score: Percent Similarity: 54.11% Conservative: 87  Best Total Similarity: 36.67% Mismatches: 154	
1229 GTGCACCACCGCTCCCCCAGCACCCACCACCATGCC	đ	ORIGIN	
582	ò		
1169 CTGCTGTTCACCATGATCTTCGTCACCTGTCCAT	අධ	frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using Mill forward and	
581	λõ	/note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading	
1109 CTGCTCATCACTGAGATCATCCCGTCCACCTCGCTC	A a	/motype="mkm" /db_xref="taxon:9606" /clore_lib="Single gene library"	
10   10   10   10   10   10   10   10	7 6	source 1zzys /organism="Homo sapiens"	
546 AspserGlyGluLysLeuGerLeuGlyvalinili 	ò €	Email: pjin@incyte.com. FEATURES Location/Qualifiers	
989 CTCATCATCCCTGCCTGCTCATCTCCTGCCTCAC	qu		
526 LeullelleProCysValLeulleAlaSerMetAla	δλ	COMMENT Contact: Jin, P.  COMMENT Contact: Jin, P.	
	qa	drug target genes AL Unpublished (2003)	
869 GCCAICGICAAIGCCACGGGCACCIACAACAGCAAA	<u> </u>	AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Young, J. and Stuve, L.L.	
486 GluLeuLeuGlyValProGlyLysArgAsnGluIle	λö		
	ପ୍ର	Homo sapiens (human) SM Homo sapiens	
	l 8		
446 AspAspGlnArgCysGluMetLysPhsGlySerTrr	δ <del>ξ</del>	LOCUS CD013901 2296 bp mRNA linear EST 21-0CT-2003 DEFINITION 90134548 Single gene library Homo sapiens CDNA, mRNA sequence.	
692 TGGGTGCCCCCGGCCATCTACAAGAGCTCCTGCAG	qu	RESULT 4	
426 TyrValProProGly1lePheLysSerThrCysLy5	δ	::: ::     	
	. A	605	
572 CTCAGGGTCCCTTCTGAGATGATCTGGATCCCCGAC	අධ	583 e	
386 LeuArglleProProHisArglleTrpLysProAsg	à		
512 CAGGAGTGGAGCGACTACAAACTGCGCTGGAACCCC	qq	572 Mer ProklaThrSerAspAlaValProLeuTrDIl	
452 GCTCAGCTCATCGATGTGTGGATGAGAAGAACCAAATC 366 LeuGluTrpAsnAspMetAsnLeuArgTrpAsnTh1	음 ò	Oy 552 SerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThr 571  bh 631 TCACTRGGTATAACAGTCGTATTGTCGCTAAGGTGTTCATGGTGTGAGGTGAAGT 690	
346 MetGlnIleIleAspValAspGluLysAsnGlnLeu	ò	Db 571 CTGATATCTGCTCTGCTGGGGTTCCTGCTTCCAGCAGACTCAGGAGAGAAGATC 630	
392 IGGGCGCCCGGIGCCCAACACTICAGACGIGGTG	qa	Qy 532 LeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeu 551	
326 LeuGluArgProValLeuAsnGluSerAspProLeu	8	Db 511 ACGATAATAATGAGGCGCAGGACTCTATACTAAGGACTTCTAATTCCCTGTGTA 570	

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roglyArgProLeuIleLeuGluPhe 608
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|CTTATCACTGGCTGGAGGAGCAACGTG 1399
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euGlnLeuSerPheGlyLeuThrLeu 345
                                                                                                nrSerAspTyrGlyGlyValLysAsp 385
                                                                                                                                                                                            alValArgAsnAsnGlySerCysLeu 425
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acattgttctctacaacaatgcagat
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ccccccarrttcccaacatcacatct
                                                                                                                                              spValLeuMetTyrAsnSerAlaAsp
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1400 GATGCCGAGGAGAGGGAG----
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US-09-303-232-2 (1-770) x AY402873 (1-1436)	Qy 312 GlulysArdLeuleuHisAsnlendenDroTvrasnThrlenGluardraff 223	21 GAGCACCGTCTATTGAGCGGCTGTTTGAGGATTACAATGAGATCATCGGCCTGTGGGCC		Db 81 AACGTGTCTGACCCAGTCATCATCCATGTTTCGAGGTGTCCATGTCTCAGGTGGAAGGTG 140	Oy 352 AspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAspMet 371	Db 141 GATGAAGTAAACCAGATCATGGAGACCAACCTGTGGCTCAAGCAAATCTGGAATGACCAC 200	Oy 372 AsnleuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHis 391	Db 201 AAGCTGAAGTGGAACCCCTCTGACTATGGTGGGGCAGAGTTCATGCTGTCCTGCTGCACAG 260	CY 392 ArgilefrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThr 411				381 TTTAAGAGGTCTCCTGTAAATCTAACAAAATCAAAAAAAA	452	Db 441 ATGAAGTTCGGTTCCTACGATAAGGCGAAAATCGATCTGGTCCTGATCGGC 497	472 ThrGlyGlyAspIleSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValPro	498	QY 492 GlyLysArgAsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspileThrPhe 511	530 GGLIACAMACACACACACACAGAGAGAGAGAGAGAGAGAGATCTACCCCGACATCACATAC			Db 678 CTCAITCCTICCACIGICICGTTTTACTGCCCTCCGACTGCGGGGAAAGGGG 737	Qy 552 SerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThr 571	Db 738 ACCCTGTGCATTTCTGTCCTCTCTCTCTGACGGTGTTTCTCCTGGTGATCACTGAGACC 797	Qy 572 MetProAlaThrSerAspAlaValProLeu	798	ογ 581 581	Db 858 TTTGTAACCTTGTCCATCGTCATCACGGTCTTCGTGCTCAACGTGCACTACAGAACCCCG 917	582	Db 918 ACGACACACACACTCTTATGGGTGAAGACTGTATTCTTGAACCTGCTCCCAGGGTC 977	595 LeuArgMetSerArgProGlyArgProLeuIleLeuGlu	978	. 615	Db 1002 AACGAGGGCAACGCTCAGAAGCCGAGGCCCCTCTACGGTGCCGAGCTCTCAAATCTGAAT 1061
ProHisAsnPro 666 US	1483	. 989	-TGCAGCCACCTGCACCTGCACTCTGGGCCTCAGGTCCCAAGGCTGAG 1531	ThrCyslleLysSerSerThr 703	1570	723	1621	AspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArg 743	1681		1738	C-2003	equence,		_	omi,		Loud, A. T. Tanenbaum, D. M., CIVello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X. H., White, T. J., Sninsky, J. J., Adams, M. D. and Cargill, M.	goos		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R., Tanenbaum, D.M., Civello, D.R.,		-	mic exons and ordering		Db Db	omic DNA" 1:9606"	qu	41369" QY			vative: ches:		ga
Qy 649 PheArgHisAsnCysArg	Db 1436 GACAGATGGGCATGTGCAGG	667 AlaPheTyrAr	Db 1484TGCAGCCA	687	1532	704 GluTyrG	1571	724	7297	Oy 744 LeuCysLeuIleIlePheTh	1682	AY402873 LOCUS AY402873	geno	AY402873.1 GSS.	SOURCE Homo sapiens (human) ORGANISM Homo sapiens		AUTHORS Clark, A.G., Glanowski, g			JOUKNAL Science 302 (5652), 1960-1963 PUBMED 14671302 REFERENCE 2 (hasset 1 to 1422)			TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics,	COMMENT This sequence was made by sequencing		/organism="Homo sapiens"		gene <1>1436 /gene="CHRNA3"	ORIGIN / Locus_tag="HC	Scores:		retcent similarity: 54.71% Best Local Similarity: 35.25% Chery Match.		

Nature 409, 685-690 (2001)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,X., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,X., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKO53497
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103El4 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                 1215 TCC------CICTCTGCTTTGTCACCAGAAATCAAAGCCATCCAAAGTGTC 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AAAGGCTGCAAG 1094
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                    635 SerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisAsnCysArg 654
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                675 GlnGlyAspAspGlySerIleGlyProlleGlySerThrArgMetProAspAlaValThr
                                                                                                                                                                                                                                                                                          695 HisHisThrCysIleLysSerSerThrGluTyrGluLeuGlyLeuIleLeuLysGluIle
                                                                                                            ProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThrValTyrGly
                                                                                                                                                           1095 GAGGGCTACCCCTGCCAGGACGGGATGTGTGTGTTACTGCCACCACCACGCAGGATAAAAATC
                                                                                                                                                                                                                                                   1155 TCCAATITCAGTGCTAACCTCACGAGAAGCTCTAGTTCTGAATCTGTTGATGCTGTGCTG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mus musculus (house mouse)
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AK053497.1 GI:26343494
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FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection

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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase 1 & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furihara, C., Sibhi, Y., Itch, M., Kagawa, T., Kacani, K., Ishi, Y., Itch, M., Kagawa, T., Kacani, K., Sibhi, Y., Itch, M., Kagawa, T., Kacani, C., Matsuyama, T., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsako, N., Okazaki, Y., Saato, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Saobe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Sakazume, N., Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Genomic Sciences Center (GSC), Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Exploration Research Group, RIKEN Genomic Sciences Center (GSC), KAINAGAWA 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, PRISE PASSER 45-503-9222, PRISE PASSER 45-503-9222, PRISE PASSER 45-503-9222, PRISE PASSER 45-503-9216)
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ITVELLVIFETIPSTISCYIPLIGEVLETMIFFYTESTVTTVFVLNWFTRPTTHIMPT
WVKAVFLINLIPRVMENTRPISTEDAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCO
DGTCGYCHHRRVKISRSANLIRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMK
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\(\frac{1}{\text{protein id="BA035404.1"}}\)
\(\frac{1}{\text{protein id="BA33495"}}\)
\(\frac{1}{\text{cranslation="WRVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFEDYNEII FRYANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIMNDYKLKWKPSDYQGVEF\)
\(\text{RPNANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIMNDYKLKWKPSDYQGVEF\)
\(\text{RPNANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIMNDYKLKWKPSDYQGVEF\)
\end{align*}
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PFDYQNCTWKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAILKAPGYKHEIKXNCC
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
94. [1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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|db_xref="MG1:4455288"
|db_xref="taxon:10090"
|clone="E130103E14"
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/strain="C57BL/6J"
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	658 ProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThrValTyrGlyGln (	716 PhelleThraspGlnLeuArgLysAspAspGluCysAsnAsGCCAICCAAAGGTGAAGG 1 716 PhelleThraspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsnAspTrpLys 7 716 Fill 11	756 AlaThrIleAlaValLeuLeu 762	Mus musculus 12 days embryo signerative cone: D13006 ACETYLCHOLINE RECEPTOR ALPHA 3 AKO51730 G1:26342155 HTC; CAP trapper. Mus musculus (house mouse)			AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
#26.50 Matches: 176  milarity: 54.04* Conservative: 98  milarity: 34.71* Mismatches: 166  20.44* Indels: 67  10.44* Indels: 67  21.44* Indels: 67  LeubeulleTyrLeuAsnLeuSeralaLysValCysLeuAladlyTyrHisGluLysArg 314  ***********************************	uLys     AGTA  :::  :::	CTGG 426  Thr 414  AACC 486  SSEr 434	GAGC 546 SPhe 454      GTTC 606 VGly 474	CAIG 663 SARG 494 SARA 723 SARA 723 SILE 514	eala 534 	ThrValPheLeuAsnMetValAlaGluThrMetProAla 574	AU  TTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACTACAGAACTCCGACCACACAC  TTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACTACAGAACTCCGACCACACAC  TTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACTACAGAACTCCGACCACACAC  TTGTCATCATCACAGTCATTGTGCTCAACGTGCACTACAGAACTCCGACCACACACA
Score:  Percent Similarity: 54.04% Best Local Similarity: 34.71% Query Match: 11 US-09-303-232-2 (1-770) x AK0534 QY 295 LeuLeulleTyrLeuAsn :::  :::  Db 127 ATGCTGATGCTGTGCTG QY 315 LeuLeuHisAspLeuLeu Db 187 CTGTTCCAGTATT	335 247 355 307 375		487 435 547 455	DD 607 GGCTCCTGGTCCTACGACR  Qy 475 ASDILESERSETTYVALI  DD 664 AACCTCAAGGACTATTGGC  Qy 495 ASDGTULETYTASDC  DD 724 CATGAAATCAAGTACAACAACAACAACAACAACAACAACAACAACAACAACA	Oy 515   leArgArgArgArgThrLeuT	Qy         555 ValThrileLeuLeuSerLeu           Db         904 ATCTCCGTGCTCCTCCCCTG           QY         575 ThrSerAspalaValProLeu           Db         964 ACCTCACTGGTCATCCCCTTG	Qy         581

TITLE

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S Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, W., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kowda, M., Kojima, Y., Kondo, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tamaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Miramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Miramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Miramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Miramatsu, M. and Hayashizaki, Y., Taya, T., Yasunishi, A., Miramatsu, M., Saito, M., Miramatsu, M., Saito, M., Saito, M., Toya, T., Yasunishi, A., Miramatsu, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., Saito, M., 
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PRDYQNCTMKREGSWSYDKAKIDLVLIGSSNNLKDYWBSGEWAIIRABCH
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LTVPLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHYRTPTTHTMPT
WYRAVFLNLLPRVMFMTRPTSTEEDAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Lastitute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
           Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                 FANTOM Consortium.
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramcto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hiramcto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kaguwa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojian, Y., Kondo, S., Konno, H., Kounda, M., Marata, M., Mishi, K., Nomura, K., Numazaki, A., Murata, M., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Saitoh, H., Sakai, C., Sakai, K., Shiraki, T., Sayazi, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission Hayashizaki, Y. Laboratory for Genome Submistion Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Rangawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suhii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Zakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3126)
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471,
evidence: FASTY, 99 8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                ACCICACTGGTCATCCCCTTGATCGGGGAGTACCTCCTCTTCACTATGATTTTTGTCACC 1099
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007P14 product:NEURONAL NICOTINIC ACETICHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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SerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeuGly
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Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (Dases 1 to 1436)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A..
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Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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1049 GCCACCTCCACCAGCCCTCCAAC 1088 cccccccrcrccacriccaagrer 1142 CAGGGATTTCTGGCTGCGGTCCTCT 1196 : :: ||||||| AGGTGTCAGCTTCATCGCCCAGCAC 1256 GTGCGTCCTGGGCACTGTGGGGGCTC 1376 3GCCAGAGCCTTCCCG------ 1028 uLeuAlaAsnValLeuAspIleAsp 646 rProGlyGlyThrLeuProHisAsn 665 yGlnGlyAspAspGlySerIleGly 682 sGluileArgPheileThrAspGln 720 nAspTrpLysPheAlaAlaMetVal 740 eAlalleLeuAlaThrIleAlaVal 760 eArgArgArgThrLeuTyrTyrPhe 523 |Thr1|eleuleuSerLeuThrVal 563 |::::::|||||||::|||||| CTCAGTGCTGCTGCACTGACATTC 773 rArgProGlyArgProLeulleLeu 606 rGluArgLysHisGlnIleLeuSer 626 CATGGATGACTTTACTCCCAGTGGT 542 rMetalaLeuLeuGlyPheThrLeu 543
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GCTGGCCATCCTCTTCTACCTG 713 ||||| crccrccargreccrcrcarces 833 CTCCATCGTCACCAGCGTCTGTGTG 893 -----TrpileArgileVal 586 CATGGCACCCTGGGTCAAGCGCTGC 953 nGluileTyrTyrAsnCysCysPro 503 A-----GTGAACCCACAGAC 593 581 581 rHisHisThrCysIleLysSerSer acaccatac-----SerAspAlaValProLeu-----CGTGACC-----)IleSerSerTyrValLeuAsnGly

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967 CCCAGCACCCAIGTCAIGCCCAACIGGGIGCGGAAGGITTITAICGACACTAICCCAAAI 1026
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310 AAGATCTGGCGCCCAGACCTTGTTCTCTATAACAATGCAGATGGTGACTTTGCTATTGTC
                                                  PheLysSerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArgCysGlu
                                                                                                         MetLysPheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGlu
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1 (Bases 1 to 1374)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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|TGGCCTCTCTCCTCCTGCTCTTAGCCTTTGCTCAGCTGGCCTCGTCCTGGGCTCCGAACAT
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CHRNA1"
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AY406230.1 GI:39762204
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Db 11  QY  QY  Db 11  RESULT 12  AY402878  LOCUS  DEFINITION  ACCESSION  KEYWORDS  SOURCE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS	TITLE JOURNAL COMMENT FEATURES SOUR Gene	Alignment Pred. No.: Score: Score: Percent Si Best Local Query Matc DB: US-09-303- Qy Db Qy Db Qy Db

Oy 311 HisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProVal 330	187 GTGGATGAAATCAGATTGTGACAACCAATGTACGTCTGAAACAGCAATGGGTCGAT 371 MetasnleuargTrpasnThrSeraspTyrGlyVallysaspLeuarglleProPro 247 TACAACTTGAAATCGAATCCAGATGACTATGGAGAGTGAAAAAAATTCACATCCCTCG			491 604 510 564	Qy         530 CysValLeuIleAlaSerMetAlaLeuLeuGlyPheThrLeuProAspSerGlyGlu 549           Db         724 TGCTGCTCTTCTCTTTAACCAGCTGTTTCTACCTGCCCACAGACTCAGGGGAG 783           Qy         550 LySLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla 569           Db         784 AAGATGACGCTGACCTGTCTTACTGTCCTGACCGTGTTCCTTCTGGTCATTCTG		Db 904 ATGGTCTTTGTCATTGTCATCATCATCACCGTCATCGTCATCACACACA	Db 1024 AACATCATGTTTTCTCCACAATGAAAAGACCA
1143 ACTCCTAAGTCTGCAGTCACCTCCCACGGCAGCCTCCCCAGGGATGCCCGGCTG 1199 700 LysSexSerThxGluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheile 717 :::        :::         1200 AGGTCCTCTGGCAGGTTCCGGCAAGATCTACAGGAAGCATTAGAGGCGTCAGCTTCATC 1259 718 ThxAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsnAspTxpLysPheAla 737	Oy 738 AlaMetValValAspArgLeuCysLeuIleIlePheThrMetPheAlaileLeuAlaThr 757	SULT 13 SULT 13 SULT 13 SULT 13 SULT 13 SULT 13 SULT 13 AY406232 AY406232 FINITION Mus musculus CHRNA1 gene, VIRTUAL TRANSCRIPT, partial sequence, GESSION AY406232 RSION AY406232 II 339762206 RSION AY406232 II (1:39762206 RSION AY406232 II (house mones) RMCE Mis musculus (house mones)	Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  (Cark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tonenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Adams, M.D. and Cargill, M.	<pre>ion from human-chimp-mouse orthologous 63 (2003) ielson,R., Thomas,P., Kejariwal,A., Civello,D.R., Lu,F., Murphy,B., .X.H., White,T.J., Sninsky,J.J.,</pre>	lera Genomics, 45 West Gude Drive, sequencing genomic exons and ordering rs	/mol_type="genomic_DNA" /db_xref="taxon:10090" /db_xref="taxon:10090" <1>1374 /gene="CHRNA1" /locus_tag="HCM2488"	Alignment Scores:  Pred. No.:  Score:  Score:  797.00  Matches:  169  Percent Similarity:  71.97  Conservative:  Mismatches:  140  Query Match:  19.71  Gaps:  104	US-09-303-232-2 (1-770) x AY406232 (1-1374)  QY 291 SerTrpIlePheLeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyr 310  Q 291 SerTrpIlePheLeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyr 310  Q 291 SerTrpIlePheLeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyr 310  D 10 TCGACTGTTCTCCTGCTGCTAGGCCTCTGCTCCGCTGGCCTTGTTCTGGGCTCCGAA 66  O C C C C C C C C C C C C C C C C C C

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L Nature 420, 563-573 (2002)

B (bases 1 to 429)

S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haramoto, K., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirozane, T., Hori, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojina, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numaza, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakai, W., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagani, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomara, Y., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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EKIMRPDVVLYNNADGDFAIVKFTKVLLDYTGHITWTPPAIFKSYCEIIVTHFPFEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken prepare mouse tissues.
                                                      based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product; cholinergic receptor,
nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885,
GB|NM_007389, evidence: BLASTN, 99%, match=1763)
The FANTOM Consortium and the RIKEN Genome Exploration Research
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95
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Matches:
Conservative:
                                 Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                            ----CCACCTATG 1140
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      713 GlulleArgPhelleThrAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspTrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPhe
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                                                                                                                                                                                                                  673 TyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArgMetProAspAla
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         1066 AAACAAGAAAAAGATTTTACAGAAGACATAGATATATCTGAC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
Mus musculus
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Best Local Similarity: 33.27% Mismatches: 140 Query Match: 19.71% Indels: 104 DB: 8	US-09-303-232-2 (1-770) x AK029177 (1-4290)	7	Db 30 réacrerrerectéchacragecereracrecenageceregeerregage 86	Oy 311 HisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProVal 330			ValAspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAsp	20/ GIGGAIGAAGTAAATCAGAITGIGACAACCAATGIACGICTGAAACAGCAATGGGTCGAT 371 Metaanlanatgitaatanthaganthagataantaantaataataataataataataa		spGly 41	4	431	Db 447 ATCTTTAAAAGCTACTGTGAGATCATTGTCACTCACTTCCCTTCGATGAGCAGAACTGC 506	OY 451 GlumetLysPheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAsp 470	Qy 471 GluThrGlyGlyAspIleSerSerTyrValLeuAsnGlyGluLrpGluLeuLeuGlyVal 490 :::            :::  Db 567 GACCAGCCCGACCTGAGTAACTTCATGGAGGAGGGGGAGTGGTGATCAAGGAAGCT 623	spile	510	684 ACCTACCATTCGTCATGCGCCTGCCCTCTACTTCATTGTCAACGTCATGCCTCCCCTCTACTTCATTGTCAACGTCATCATTCCC	Oy 530 CysValleulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu 549	550 LysLeuSerLeuGlyValThrlleLeuLeuSerLeuThrValPheLeuAsnMetValAla	Db 804 AAGAIGACGCTGAGCATCTCTGTCTTÄCTGTCCTGACGGTGTTCCTTCTGGTCATTGTG 863 QY 570 GluthimetProalathisSexAspAlaValProLeu	:::   :::	Qy 581 581	924 AIGGICTTIGICATIGCGICCAICATCAICACGICAICGICAI	OY 582

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	894 CTCANTGTGCACC
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306 CysLeuAlaGlyTyrHisGluLysArgLeuLeuHisAspLeuLeuAspProTyr 3	н
AsnThrLeuGluArgProValLeuAsnGluSerAspProLeuGlnLeuSerPheGlyLeu	1041
66 AATAACCTGATCCGCCCAGCCACCAGCTCCTCACAGCTCATCATCATCAAGCTGCAGCTC 123	663 ProHisAsnProA
TCCCTGGCCCAACTTATCAGCGTGAATGAGCGAGAGCAGATCATGACCACCAATGTCTGG	н
364 LeulysLeuGluTrpAsnAspMetAsnLeuArgTrpAsnThrSerAspTyrGlyGlyVal 383	Db 1134 TCCAAGTCTCCAGCCGCNNTAC
186 CTGAAACAGGAATGGACTGATTACCGCCTGACCTGGAAACAGCTCCCGCTACGAGGGGGTGTG 24	700
384 LysAspLeuArgIleProProHisArgIleTrpLysProAspValLeuMetTyrAsnSer 403	-
	Qy 718 ThrAspGlnLeuArgLysAspAsp
404 AlaAspGluGlyPheAspGlyThrTyrGlnThrAsnValValValArgAsnAsnGlySer 423	1248
424 CysLeuTyrValProProGly1lePheLysSerThrCysLysIleAspIleThrTrpPhe 443	Oy 738 AlaMetValValAspArgueuCyS
366 GTCCTGTGGCCTGCCCTGCCATCTACAAGAGCGCCTGCCAAGATTGAGGTGAAGTTT 42:	758
444 ProPheaspaspGlnargCysGluMetLysPheGlySerTrpThrTyraspGlyPheGln 463	1368
464 LeuAspLeuGlnLeuGlnAspGluThrGlyGlyAspIleSerSerTyrValLeuAsnGly 483 :::	Search completed: May 9, 2004 Job time : 5420.49 secs
484 GluTrpGluLeuLeuGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCysPro 503	
504 GluProTyrIleAspIleThrPheAlaIleIleIleArgArgArgThrLeuTyrTyrPhe 52	
594 CCCAGCTACGTGACGTACACTTCATCATCAAGCGCAAGCCTCTGTTCTACACC 653	
524 PheAsnLeullelleProCysValLeulleAlaSerWetAlaLeuLeuGlyPheThrLeu 543	
544 ProproAspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrVal 563	
564 PheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAlaValProLeu 58:	
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SCGTNACCAAGCCCACCACCTNNNCAGT 1079 spGluCysAsnAspIleAlaAsnAspIrpLysPheAla 737 ||||:::||| |Carcagcagcagagccttc----- 1025 rSerLysSerLeuLeuAlaAsnValLeuAspIleAsp 646 gProMetThrProGlyGlyThrLeu------ 662 -ArgThrValTyr-----GlyGlnGlyAspAspGly 679 rArgMetProAspalaValThrHisHisThrCysIle 699 -GluLeuGlyLeulleLeuLysGlulleArgPheile 717 sieullellepheThrMetPheAlalleieuAlaThr 757 rAspThrserSerGluArgLysHisGlnIleLeuSer 626 INCTGGTCACCTTCTCCATCGTCANNAGCGTCTGTGTG 893 ---TrpileArgileVal 586 eleuArgMetSerArgProGlyArgProLeulleLeu 606 

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## ALIGNMENTS

	AF143846 3629 bp mRNA linear TNV 27-MAY-1999	Heliothis virescens puta	7-1 subunit mRNA, complete cds.		AF143846.1 GI:4895004		Heliothis virescens (tobacco budworm)		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;	Noctuoidea; Noctuidae; Heliothinae; Heliothis.			
RESULT 1 AF143846	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	

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VTILLSLTYPELMWARETMPATSDAVPLGTYFNCINEWVASSVVSTILLLNYHHRHAD
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100.0%; Score 1488; DB 3; Length 3629;
Best Local Similarity 100.0%; Pred. No. 7.2e-291;
Matches 1488; Conservative 0; Mismatches 0; Indels 0;
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/product="putative nicotinic acetylcholine
7-1 subunit"
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2 (bases 1 to 3629)
Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, 51368, Germany
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/organism="Heliothis virescens"
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/db_xref="taxon:7102"
335. 1825
/note="hvnachra7-1"
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                                                         TITGICACGAATGGCGAATGGGAGTTAATAGGAGTCCCCGGCAAGCGCAACGAGATCTAC
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3701 bp DNA linear PAT 18-JUN Nucleic acid encoding insect actyl choline receptor subunit. E58347.1 GI:13019346
JP 2000023680-A/2.
Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
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THEMSDWIRCVFLYMLPWYLRMSRPGSATTPPPARVPPPPDLELRERSSKSLLANVLD
IDDDFRHPQAQQPQCTRYRGGEENGAGLAAHSCFGWDYELSLILKRITVJTDQMRKD
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                                                                                                                                              Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 3 08-DEC-1999;
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                                 Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Noctuoidea, Noctuidae, Heliothinae, Heliothis.
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100.0%; Pred. No. 7.2e-291;
ive 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:7102"
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctucidea; Noctuidae; Heliothinae; Heliothis.  1 (bases 1 to 3701) AUTHORS MARITHA,A., Madia,E. and Thomas,S. TITLE Nucleic acid encoding insect actyl choline receptor subunit BAYER AG COMMENT PA 19200023680-A 2 25-JAN-2000; BAYER AG COMMENT PN JP 2000023680-A/2 PD 25-JAN-1999 PR 04-MAY-1999	FH Key Location/Qualifiers FT CDS (335). (1822). Source 1. 3701 / organism="Heliothis virescens" / mol_type="genomic DNA" / db_xref="taxon:7102"	aps  GCCCC  GCCC  GCCC  GCC  GCCC  GCCC  GCCC  GCCC  GCCC  GCCC  GCC  GCCC  GCCC  GCCC  GCCC  GCCC  GCC  GCC  GCCC  GCCC  GCC  GCC  GCCC  GCCC  GCC  GCC  G	

13   Store 615; DB 3; Length 2023;   Lest Local Similarity 64.6%;   Pred. No. 3.7e-114;   Length 2023;   Latches 950;   Conservative 0;   Mismatches 515;   Indels 6;   Gaps 2;   CTCGCACTTGGCGGCCCGGGGCCTGCTGCTGCTGCTGCTCTGGCGGGGG 80	201 CATGGGACCCGTGGCCAATGAATCGGAGCCCTTGGATAAGTTCGGACTGAAGCT 566 201 CATGCAGATCACCGCGAGGAGGAGGAGGACTTAATAACAAACA	GTACGTCCCCCCCCCCCCCCTTCTAAAACCACCTCCCAAAATACCCCCTTTTTCTAAAATCCCAAAATCCCAACATCCCCTTTTTT		
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Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.  Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002) 11973307 11973307 2 (bases 1 to 2023) Grauso, M. and Sattelle, D.B. Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1	UK Location/Qualifiers 12023   organism="Drosophila melanogaster"     /mol_type="mRNA"     /mol_type="mRNA"     /db_xref="taxon:7227"     /db_xref="taxon:7227"     /dwy stage="embryo"     12023     /gene="nAcRalpha-30D"     /gene="nAcRalpha-30D"     /gene="nAcRalpha-30D"     /gene="nAcRalpha-30D"     /gene="nAcRalpha-30D"     /gene="nAcRalpha-30D"     /gene="nacRalpha-30D"	Januar (12 pe 11)  Jarcel="G1:20152847"  / db_xref="G1:20152847"  / db_xref="G1:20152847"  / tanslation="MDSPLPASISLFVLLIFLAIIKESCQCPHEKRLINHLLSTYNTL  / kranslation="MDSPLPASISLFVLLIFLAIIKESCQCPHEKRLINHLLSTYNTL  / kranslation="MDSPLPASISLFVLLIFLAIIKESCQCPHEKRLINHLLSTYNTL  / kranslation="MDSPLPASISLFVLLIFLAIIKESCBADISCHEKSTCKMDITW  / propoper (12 per propoper per per per per per per per per per	/replace="aa" 794 /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /note="results in glycine to serine substitution; compared to variant clone" /replace="a" 846 /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /mote="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession /wmber AB5005c26 and in variant clone" /replace="a"	1314 /gene="nAcRalpha-30D" /note="compared to variant clone" /replace="a" /gene="nAcRalpha-30D" /replace="to variant clone" /note="nAcRalpha-30D" /note="nAcRalpha-30D" /replace="to variant clone"
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DLRITPNKLMKEDVLMYNSADEGFDGTYHTSVVVKHGGSCLYVPPGIFKSTCKMDITW
PFDDQHCEMKFGSWTYDGNQLDLVLSSEDGGDLSDFTINGEWYLLEMPGKKRTIVYA
CCPEPVYTTLQIRRRLLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGYTLL
LSLTVPFLNLVABSEMPTFSDAVPLIGTYFNCINFWVASSVVLTVVVLNYHHRTADIHEM
PWIKSVFLQMLPWILLRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
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/db_xref="GI:29466435"
/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha6 (nAcRalpha-30D gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WCIE 6BT, UNITED
CGCCATTGGCTCGTCGGCCAGCTTCGGTCGGCCCACACGGTGGAGGAGCATCACACGGC
                                                                                          AATACTATTAAGCAATCGCATGAAGGAGCTGGAGCTAAAAGGAGCGCTCCTCCAAAATCCCT
                                                                                                                              CCTAGCGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCA
                                                                                                                                                                                                   CTTCGGTGTCG---ACTACGAGCTCTCCCTCATTCTGAAGGAGATTAGAGTCATCACAGA
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                                                        GGCGCGCGTA----CCTCCGCCGCCCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCT
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Dalpha6"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epydroidea; Drosophilidae; Drosophila.
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Millar,N.S.
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nAcRalpha-30D gene; nicotinic acetylcholine receptor
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/db_xref="taxon:7227"
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reflect accurately this particular CDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site changefruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLSSEDGGDLSDFITNGEWY
LLAMPGKKNTIVYACCPEPYVDITFIQIRRRTLYYFRNLIYPCVLISSMALLGFTLP
PBGGSKLILGVTILLSLTVFLNLVABSMPTTSDAVPLIGTYFNCIMFWVASSVVTTVV
VLNYHRTADIHEMPPWIKSVFLQWLPWILMGRFGRKITRKTILLSNRWKELELKER
SSKSILAANVLDIDDFFRHTIGSSQTALGSSASFGRRPTYVEEHHTAIGCNHKDLHLILK
ELQFITARNMKADDFAHTIGSSQTALGSSAFCRPTYVEEHHTAIGCNHKDLHLILK
ELQFITARNMKADDFAHTIGSSQTALGSSAFCLIVFTLIIATVTVLLSAPHIIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="PFNPRATRYKQAKDMDSPLPASLSLFVLL1FLAIIKESCQCPHB
KRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLWLSLEWND
YNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYHTSVVVKFGGGSCLYVP
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Pred. No. 1.6e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="GH15518p"
/protein_id="AAR82815.1"
/db_xref="G1:40216008"
/db_xref="FLYBASE:FBgn0032151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="nAcRalpha-30D"
'db_xref="FLYBASE:FBgn0032151"
                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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                                                 CTTCAATTGCATCATGTTCATGGTCGCTCGTCGTGGTGCTGACAGTAGTGGTGGTCGAA
             CTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAA
                                                                                                                    CTACCACCACGCACGCACACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCT
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1699)
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Lawrence Berkeley National Laboratory, One Cyclotron Road,
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GH15518 full insert cDNA.
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laborat
Berkeley, CA 94720
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1 (bases 1 to 2023)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putarive Nicotinic Acetylcholine Receptor Subunit Genes, New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
  Ar321447 29-APR-20 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AB003626"
/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
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in GenBank Accession Number
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llarity 64.4%; Pred. No. 1.6e-113;
Conservative 0; Mismatches 517;
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to the sequence deposited
AE003626"
                                                                                                                                                                Drosophila melanogaster (fruit fly)
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/protein_id="AAM13394.1"
/db_xref="GI:20152849"
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gene="nAcRalpha-30D"
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179. .1863
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/db_xref="taxon:7227"
/chromosome="2"
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/dev_stage="embryo"
1. .2023
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Grauso, M. and Sattelle, D.B.
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Best Local Similarity
Matches 948; Conserv
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AUTHORS
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                                                                CGACGACCAACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGA
                                                                                                   532 TCATGACCAACATTGCGAAATGAAATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGA
                                                                                                                                             TCTACAACTACAGGATGAAGGGGGGGGGGAATATAAGCAGTTTTGTCACGAATGGCGAATG
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DFRHTISGSQTALIGSSASFGRPTTVERHTALGCHKOLHILIKELQFITARMRKADD
EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
  product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                   ERPVANESEPLEVKFGLTLQQIIDVDEKNQILTTNAMLNLEMNDYNLRMNETEYGGVK
DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITW
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                                                                                                                                                                                                                                                                                                           /note="results in asparagine to glycine substitution, compared to variant clone" /replace="gg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="results in asparagine to serine substitution;
compared to variant clone"
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/note="results in isoleucine to methionine
compared to variant clone"
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/replace="t"
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.2e-113;
es 519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 608.6; D
Pred. No. 7.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="compared to variant
                   variant type I"
/protein_id="AAM13392.1"
/db_xref="G1:20152845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="results in serine
                                                                                                                                                                                                                                                                                            gene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="nAcRalpha-30D"
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Best Local Similarity 64.3%;
Matches 946; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace="g'
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substitution;

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1393 AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA 1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1333 ATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGG 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1633 CGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATTA 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTG 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 CAGGATGAAGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATA 630
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                                                                                                                                                                                                                                                                                                                /note="results in deletion of asparagine and serine;
compared to B allele"
/replace=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="results in asparagine to serine substitution;
compared to B allele"
/replace="g"
                                                                                                                                                                                                                  /note="results in lysine to argenine substitution;
compared to B allele"
                                                                                                                                                                                                                                                                                                                                                                                                 /note="results in serine, glycine, and asparagine insertion; compared to B allele" /replace="agoggcaac" 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2907;
      /note="results in phenylalanine to isoleucine substitution; compared to B allele" /replace="c"
                                                                                                                 to isoleucine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.7e-108;
0; Mismatches 422;
                                                                                            /gene="nAcRalpha-34E"
/note="results in threonine
compared to B allele"
gene="nAcRalpha-34E"
                                                                                                                                                                                             /gene="nAcRalpha-34E"
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                                                                                                                                                    AF272778 29-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha-34E) mRNA, nAcRalpha-34E-A allele, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="G1:20152840"
/translation="MKNAQLKLIEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRH
NQQLTTLQPRSLSTKHHSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSS
                                                                                                                                                                                                                                                                                                                                                                                      Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RAN-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chases 1 to 2907)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OXI 3QX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="ion channel; neurotransmitter transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="nicotinic acetylcholine receptor Dalpha5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                                       1827 GGTGCTCTCCGCTCCGCACATAATCGTG 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="nAcRalpha-34E"
/note="compared to B allele"
/replace="a"
375
                CGTGCTGCTGTCCGCGCCACACATCATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein id="AAM13390.1"
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/gene="nAcRalpha-34E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="nAcRalpha-34E"
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L. .2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="2L; 34E4-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="2"
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SOURCE
ORGANISM
                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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MEDLINE
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AUTHORS
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4.

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1272

150

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270

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuoidea; Heliothinae; Heliothis.

1 (bases I to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLWKDDVLMYNSADEGFDGTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQH
CDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLLGMPGKKNTITYACCPEPYV
DVTFTIMIRRATLYYPFNLIVPCVLLSSMALLGFTLPPDSGGEKLTLGVTTLLSSLYFF
NLVABTLPQVSDAIPLIVFYNCINFWVASSVVLTVVVLNYHRTADIHBMPQMIKSV
FLQWLPWILRNGSFGKKITRKTIMMTYRMELELKERSSKSLLANVLDIDDDFRHGFP
PPNSTASTGNLGFGCSIFRTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRELQFITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mapmlaalallalledgephekrllnallanyuterpvane
Seplevregitilootidddeknollitniwlslewndynlrwndseyggvkdlritpn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="putative nicotinic acetylcholine receptor alpha
7-2 subunit"
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Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-AFR-1999) ZF-BTB, Bayer AG, 51368, Germany
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|mol_type="mRNA"
|db_xref="taxon:7102"
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DEFINITION ACCESSION VERSION KEYWORDS

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(bases 1 to 310)

Martin,A.; Nadja,E. and Thomas, S.

Muclia; acid encoding insect actyl choline receptor subunit. Patent: JP 2000023680-A 3 25-JAN-2000;
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PN TP 2000023680-A/3

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PF 26-APR-1999 UE 1999118159

PR 04-MAY-1999 UE 1981829.9

PI MARTIN ADAMUTSUEUSUKI, NADJA ERASU, THOMAS SCHULTE PC (21201/68), 10115/09, 20115/09, 20115/09, 20115/09, 20115/09, 20115/09, 20115/00, C12N1/21, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19), C12N15/10, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, C12N15/19, 
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Pred. No. 4.6e-106;
0; Mismatches 460; Indels
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/organism="Heliothis virescens"
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/db_xref="taxon:7102"
Heliothis virescens (tobacco budworm)
Heliothis virescens
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	/organism="Heliothis virescens" /wol_type="unassigned DNA" /db_xrefe"taxon:7102" 95. 1600		/ db_xtef="REMTREMBL:CAC07501"  / translation="MAPMLABALLALVSEQGPHEKRLINALLANYNTLERPVANE SEPLEVRFGLTLQQ1IPDVDEKNQLLITNIALSLEMNDYNLAWNDSBYGGVKDLRITPN KLWKPDVLMYNSADEGFDGTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAMFPFDDQH	CDMKEGSMTYDGNQLDLVLKDEAGGDLSDFTNGFWYLIGMGGKKWYITYACCPEPYY DVIFTIMIRRRTLYYFFNLINCYVLISSMALLGFTLPPDSGEKLTLGVTTLLSLTVFL NLVAETLEQVSDA.PELLGTYFNCINFWVASSVVLTVVVLNYHHRTADITHEMPQWIKSY FLQWLPWILRMSRPGKKITRKIIMMNTRMRELELKERSSKSLLANVLDIDDDFRHGPP	PPNSTASTONLGPGCSIFRTDFRRSFVRPSTMEDVGGGLGSHHRELHLILRRLQFITA RMKKADEEAELISDWKFAAMVUDRFCLFVFTLFTIIATVAVLLSAPHIIVQ" ORIGIN	Query Match 38.6%; Score 575; DB 6; Length 3109; Best Local Similarity 64.6%; Pred. No. 4.6e-106; Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;	OY 97 CACGAGAAGCGGCTACTGCACCACTATTGGACCACTACAACGTACTGGAGAGGCCCGTC 156	OY 157 GTCAACGACGGCCTGCAGCTCTCCTTCGGCCTCATGCAGATCATCGAC 216	QY 217 GTGGACGAGAACCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGTGGAATGAT 276	Qy 277 atgaacttgaggtggaacacttcagatttcggcgggggtcaaagatttaagagtgccaccc 336	Qy 337 CACAGACTATGGAAACCAGACGTCTTATGTACAACAGCGGGGCGGACGAGGGTTCGACAGC 396  198 AACAAGTTGTGGGAAGCCGGACGTCCTTATGTATAGTGCTGACGAGGGTTTTGACGGG 457	QY 397 ACGTATCCAACGAGGGGGGGGGACAACAACGGCTCGTGTCTGTACGTGCCGCCCGGC 456	QY 457 ATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACGATGG 516	OY 517 GAGALGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGATCTACAACTACAGGAT 576
697 ITTGCGGTGGTGATCCGGAGGAAACGCTCTACTTCTTCAATCTGATCGTGCCCTGC 756	757 GIGCICAICGCCICCAIGGCICIATIGGGGIICACCTIGCCTCCAGACICCGGAGAAAG 816 	817 ITGICITIAGGIGIGACGANATIACIGICGITICACCAGACGAGATACCAGACGGGGGGGGGG	877 ACGATGCCAGGACGTCGGACGCCGTGCCCTTGCTCGGCACCTACTTCAACTGCATCATG 936	937 ITCATGGTGGCTTCCTCCGTCGTCTCCACCATGCTGATCTACCACCACCGGCAC 996	997 GCAGACACTCACGAAATGAGTGATTGGATTGGTGTTTCCTTTATTGGCTGCCGTGG 1056	1057 GTGCTGCGCATGTCACGGCCCGGCTCGGCGACGACGCCGCCGCCGCGCGCGCGTACCT 1113		TGCCG	ATACTACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TCATT 13	ACATT		TG 146	

> PAT 06-SEP-2000 Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
> Nucleic acids encoding acetylcholin-receptor subunits from insects
> Patent: EP 0962528-A 5 08-DEC-1999; Heliothis virescens (tobacco budworm)
> Heliothis virescens
> Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
> Neoptera; Endopterrygota; Lepidoptera; Glossata; Ditrysia;
> Noctuoidea; Noctuidae; Heliothinae; Heliothis. linear DNA AX009614 3109 bp Sequence 5 from Patent EP0962528. AX009614 AX009614.1 GI:9996846 RESULT 12
> AX009614
> LOCUS
> DEFINITION
> ACCESSION
> VERSION
> KEYWORDS
> SOURCE
> ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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                                                                                                                              crcacacrrddagrcacrarrcrrcracdcrdadgrdrrccrcaaccrdgradccdag 937
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                                                                  TIGICITIAGGIGIGACGATATIACIGICGIIGACGGIGITCCICAACAIGGIGGCGGAG
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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WCIE 6BT, UNITED
                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                             subunit
                                                                                        nAcRalpha-18C gene; nicotinic acetylcholine receptor
                        Drosophila melanogaster mRNA for nic
subunit Dalpha7 (nAcRalpha-18C gene)
                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1683
                                                           AJ554210
AJ554210.1 GI:29466436
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                                                       ACCESSION
VERSION
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730

GGTGTGCCCGGTAAACGAAATGAAATCTACTATAATTGCTGCCCAGAACCTTATATTGAC

671

source

FEATURES

AUTHORS JOURNAL

REFERENCE

KEYWORDS

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/db_xref="G1:29466437"
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                                                                                                                                              'product="nicotinic acetylcholine receptor subunit
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/gene="nAcRalpha-18C"
/product="nicotinic acetylcholine
Dalpha7"
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Pred. No. 9.9e-105;
0; Mismatches 416;
                                              gene="nAcRalpha-18C"
                                                                                             /gene="nAcRalpha-18C"
db <u>x</u>ref="taxon:7227"
                                                                                                                codon_start=1
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AF321448.1 GI:20152850  Drosophila melanogaster (fruit fly)  Drosophila melanogaster  Drosophila melanogaster  Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;  Ephydroidea; Drosophilae; Drosophila.  I (bases i to 2068)  Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.  Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,  Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on		Genetics Unit, University of Oxford, 3QX, UK Location/Qualifiers 1. 2068 /organism="Drosophila melanc/mol_type="mRN4" /db_xref="taxon:7227" /chromosome="2"	/map="30D1" /dev_stage="embryo" 12068 12068 /gene="nAcRalpha-30D" /gene="nAcRalpha-30D" /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a, 3b	8b; contains two repeats of the functional domain loop D"  /codon_start=I" /product="nicotinic acetylcholine receptor Dalpha6 subunit variant type IV" /protein id="AAM13395.1" /db_xref="I01:2015281" /translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHILSTYNTL ERPWARESPELEVKFGLTLQQIIDVDERWQLLITHANINDERQQLAITHINGSLEWN ERPWARESPELEVKFGLTLQQIIDVDERWQLLITHANINDERQQLAITHINGSLEWN		variation 836 /gene="nAcRalpha-30D" /note="results in arginine to histidine substitution; /compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" variation 839 ""	/gene="nackapna-sup" /note="results in serine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" variation 891	/gene="nAcRalpha-30D" /note="results in methionine to isoleucine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" /replace="a" /ass /gene="nAcRalpha-30D" /note="compared to the sequence deposited in GenBank
VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE	gene			var:	var	Var
QY         691 ATCACGTTGCGGTGGTGATCCGGAGGAAACGTTCTACTACTTCTTCATCTGTTCGT         750           Db         731 ATAACATTCGCCATTTGATAAGGCGCAAAACGTTGTACTTTTTTCAATCTGATTGTG         790           QY         751 CCCTGCGTGCTCTTTGGTCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGA         810           Db         791 CCGTGCGTGCTCATGGCTCTATTGGGGTTTACACTGCCACACATCTGGT         850           QY         811 GAAAAGTTGTCTTTAGGTGTGACATTATTACTGTTGACGGTTCCTCAACATGGTG         870           Db         851 GAAAAGTTTCGTTGAGATTACAATTCTATTATCGCTTACAGTCTTCCTCAACATGGTG         910	QY         871 GCGGAGACGACGACGACGCCGACGCCGTGCCTCGGCACCTTCTCAACTGC 930           Db         911 GCCGAAACAATGCCGGCGACCTCCGATGCGGTACGCTGCTCGGTAAGTATTTCAATTGC 970           QY         931 ATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCCGATACTGATCCTCCACCACCACCACCACCACCACCACCACCACCACC	QY         991 CGGCAGACACTCACGAAATGAGTGATTGGATTGGTTGCTTTATTGGCTG 1050           Db         1031 AGAAATCCAGATACGCATGAATGAGTGAATAGAGTAATATTCCTTTATTGGTTA 1090           QY         1051 CCGTGGGTGCTGCGATGTCACGGCCCGGCTCGGCGACGACGCCGCCG 1101           Db         1091 CCTTGCATATTGCGCATGCAAAGACCCGGACGAGGTTGGCTACGAATGTCCGCCGCCC 1150	QY         1102 GCGCGCGTACCTCCGCCGG	QY         1195 CAC	QY         1291        TACGAGCTC 1299           Db         1391         GGGCGTTTGCACGAGGCCATTTCCCACCTGTCTGACATCTGGGGAGTACGAGTACGAACTG 1450           QY         1300         TCCCTCATTCTGAAGGAGATTAGAGTCATCACAGATCAGATGGGCAAGGACGACGAAGAT 1359           Db         1451         GCGCTGATACTCAAGGAGTTGATAACAGAACAGCTCAAAAAAAGAGGAACACAGAAACA 1510	TATT		RESULT 14 AF321448 LOCUS AF321448 LOCUS AF321448 DEFINITION Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type IV (nAcRalpha-30D) mRNA, complete cds, alternatively spliced. ACCESSION AF321448

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Accession Number AE003626"
1728
                                                                                                                                  /note="compared to the sequence deposited in GenBank
Accession Number AE003626"
/replace="c"
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                    Length 2068;
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                                                                                                                                                                                                                 Score 553.6; DB 3;
Pred. No. 9.8e-102;
0; Mismatches 519;
Accession Number AE003626"
                                                                                                                     'gene="nAcRalpha-30D"
                                                                                                                                                                                                                37.2%;
ilarity 62.4%;
Conservative
             /replace="c"
1605
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Best Local Similarity
Matches 946; Conserv
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QY  QY  QY  QY  DD  QY  QY  QY  QY  QY
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FERTINGS 2 (bases 1 to 2110)  ATTHORNS OF ALL AND STATES IN THE STATE OF THE STATES IN	507 GCTGGAGCGACCGTGGCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCT 566 201 CATGCAGATCATCGACGAGGAGAAGCAGCTTTTAATAACAAACA		321 TTTAAGAGTGCCACCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGGGGGGG 380	381 CGAAGGGTTCGACAGCACGTATCCAACGACGGGTGGTGCGGAACAACGGCTCGTGTCT 440	747 TGAGGGATTCGATGGCACGTATCACACATGTGGGTCAAACATAACGGCAGTTGTCT 806	441 GTACGTGCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTT 500	501 CGACGACCAAGATGGAAGGAAGGAGCTGGACTTATGATGGTTATCAGTTGGA 560 	561 TCTACAACTACAGGATGAAGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATG 620	GGAGTTAATAGGAGTCCCCGGCAAGGAGGATCTACTACAACTGTTGCCGGAGCC 68	681 ATACATCGACATCACGTTGCCGTGGTGCTCCCGGGGAAACGCTCTACTACTTCTTCAA 740 	TCTGATCGTGCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCC 800	801 AGACTCCGGAGAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTCGTTGACGGTGTTCCT 860	861 CAACATGGTGGGGGAGACGATGCCAGCGACGTCGGACGCCG	AAACCTTGTCGCCGAGTCCATGCCGACACGTCGGATGCTGTTCCTCTTATAGGAGTTAC 128	1287 AATTCTTCTATGGCTCACAGTGTTTCTCAACCTTGTAGCTGAACATTGCCCCAAGTATC 1346  902TGCCCTTGCTCGGCACCTACTTCAACTGCATGATGGTGGCTTCCTC 953  1347 TGATGCAATGGTAAGGACCTACTTCAATTGCATCATGTTCATGGTGCTCTC 1606			GCCCGGCTCGGCGAGACGACGCCGCCGCGGCGCGTACCTCCGCCGCCGGACCTGGA 113	GCTGCGCGAGCGCTCCTCCAGTCCTCTAGCGAACGTGCTCGACATT 119	
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ं उस के ज ज	1 to 2110) Satelle,D.B. Smission (15-NOV-2000) Human Anatomy and Genetics-Functional Jnit, University of Oxford, South Park Road, Oxford	Location/Qualifiers 12110 //organism="Drosophila /moltype="mRNA"	/db xref="taxon:7227" /chromosome="2" /map="30D1"	/dev_stage="embryo" 12110 //oroc_HardPaharasonH	/gene= ind.craiping-30D 379 - 1150 /cene=#acRalnha-30D#	te="ion channel; neurotransmitter transmembrane eptor; alternatively spliced; contains exons 3a, 8a contains two repeats of the transmembrane TM2 region	/codon_start=1 /product=inctinic_acetylcholine_receptor_Dalpha6_subunit variant_type V" /protein_id="AAM13396.1"	/db_xref="G1:20152853" /translation="MDSPLPASLSLPVLLIFLATIXESCQGPHEKRLINHLLSTYNTL ERPVANESEBLEVKFGLITIQUITUDEKNQILTTNAMINLEMNDYNLRWNETEYGGVK	DERT TERKLAND UMTIN SALBGE BOT THIN IV VERGET PEFEL FELCHOLIN FPERDOGHERMEGSHTYDGROLDLULUNSEDGGDLSPET TNGRWYLLAMPGKKRYTIVYA CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTILGVTIL LSLIVFLKINLARSMPTTSDRVPLIGYTFILLSLTVFRILVARFILDVSSDR PLLGGTYFN CTMFWYASSVVLIVVVLNYTHRTADIHEMPPWIKSYFLUOWLDMIPWILRWGRPGRKITRKT		/gene="nAckalpha-30D" /note="results in methionine to isoleucine compared to the sequence deposited in GenBa Number AE003626"	<pre>/replace="a" 1401 1401 /gene="nAcRalpha-30D" /note="compared to the sequence deposited in</pre>	Accession Number AE0036 /replace="c" 1647 /	quence deposited in	1770 /gene="nAcRalpha-30D" /note="compared to the sequence deposited in GenB Accession Number AE003626"	34.9%; Score 519.6; DB 3; Length	Similarity 61.0%; Fred. No. 7.58-95;  1; Conservative 0; Mismatches 514; Indels 93; Gaps CTCGCACTTGGCGGCGCCGCGGCCTGCTGCTGCTGCTGCTGCTGCT	CCGCTGCCGGCTGCTCGCTGTTTGTCCTTTGTTTTTTTT	ABGCTGTCAAGGACCTCTATGAAAGCGCTGCTGAACCATCTGCTGTCACCTAAATAC ACTGGAGAGGGCCGTCGTCAACAGAGCGACCGCACCTGCAACCTTCGCTCTCGACCTGCAAGCCTGAAAACCTTCGAAAAGCTTCGAAAAAACCTTCGAAAAAACTAAAAAAAA	

Search completed: May 8, 2004, 02:41:22 Job time : 5903.18 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model nucleic search, nucleic

7, 2004, 10:08:00 ; Search time 598.456 Seconds May Run on:

(without alignments)
10562.710 Million cell updates/sec

US-09-303-232-3\_COPY\_335\_1822 1488

Title: Perfect score:

1 atgggcgggcggcgccg..........cgccacacatcatggtgtcg 1488 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues Searched:

6747726

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

N. Geneseq 29Jan04:\*

1: geneseqn1980s:\*
2: geneseqn290s:\*
3: geneseqn2001s:\*
4: geneseqn2001as:\*
5: geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	1 4 1 1 2	viresc	melano	Drosophil	Drosophil	Wild-type	Neuronal	Human neu	Human nen	Human neu	Human neu	Human PRO	Mutant hu	Mutant hu	Mutant hu	V274T var	Human pol	Neuronal	Neuronal	an neu	ha 2 s	an neu	an nen
ion			Ö.			_				_	_		-	_	_	-	_			Human	'Alpha		Human
Description	AAZ24476	Aaz24477	Aaz24475	Ab113733	Ab107231	Aac90380	Aat 48239	Ada10864	Aav12197	Abs54875	Abv73248	Aac58395	Aac90385	Aac90386	Aac90387	Aav44687	Abz11298	Aat59196	Aat59197	Aav12199	Aaq90387	Abs54870	Abv73243
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% Query Match	100.0	38.6	34.5	31.6	30.8	27.3	27.3	27.3	27.2	27.2	27.2	27.2	27.2	27.2	27.0	26.5	26.0	22.0	21.0	20.8	20.8	20.8	20.8
Score	1488	575	512.8	470	458.2	405.6	405.6	405.6	405.2	405.2	405.2	404	404	404	402.4	394	386.8	327.4	312.2	309.2	309.2	309.2	309.2
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Aat48235 Neuronal	Abk92165 Prostate	Ada10854 Human neu	Adc71170 Human 209	Adc71168 Human 20	Abl07799 Drosophi	Aat48236 Neuronal	Ada10856 Human neu	Aac90382 Chimeric	Adb78675 Human nie	Adb78664 Human nic	Adb78674 Human nic	Adb78676 Human nic	Aad26345 Human mut	Adb78665 Human nic	Adb78666 Human nic	Adb78678 Human nic	Aas91552 DNA encod	Aat59527 Alpha4 su	Abs54871 Human neu	Abv73244 Human neu	Aav12200 Human neu
AAT48235	ABK92165	ADA10854	ADC71170	ADC71168	ABL07799	AAT48236	ADA10856	AAC90382	ADB78675	ADB78664	ADB78674	ADB78676	AAD26345	ADB78665	ADB78666	ADB78678	AAS91552	AAT59527	ABS54871	ABV73244	AAV12200
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20.8	20.8	20.8	20.8	20.8		19.6	19.6	19.5	19.5	19.5	19.4	19.4	19.3	19.3	19.3	19.3	19.2	19.2	19.2	19.2	19.2
309.2	309.2	309.2	309.2	309.2	•	292	292	9	289.8	289.8	288.2	288.2	æ	286.6	286.6	86.	286.2	286.2	285.2	285.2	285.2
4	25	26	27	8	63	0	31	32	33	34	35	36	37	38	9.0	0 #	11	42	43	44	5

## ALIGNMENTS

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                      H. virescens acetyl-choline receptor DNA from clone Hva7-1.
                                                                                                                   /*tag= a
/product= "acetyl-choline receptor"
             BP
             AAZ24476 standard; cDNA to mRNA; 3700
                                                                                                     Location/Qualifiers 335. .1825
                                                                                                                                                                  98DE-01019829.
                                         (first entry)
                                                                                        Heliothis virescens.
                                                                                                                                        DE19819829-A1
                                                                                                                                                                  04-MAY-1998;
                                        17-FEB-2000
                                                                                                                                                     11-NOV-1999
                          AAZ24476;
                                                                                                     Key
RESULT 1
       AAZ24476
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98DE-01019829 04-MAY-1998;

(FARB ) BAYER AG.

Schulte T; Adamczewski M, Oellers N,

WPI; 2000-014207/02. P-PSDB; AAY50815.

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim 1a; Page 14-17; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as

1020

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GTGCCCTTGCTCGGCACCTACTTCAACTGCATCATGTTCATGTTGATGCTTCCTCCCCTCGTC
                                            TCCACCATACTGATCCTCAACTACCACCACCGGCACGCAGACACTCACGAAATGAGTGAT
                                                                   TCCACCATACTGATCCTCAACTACCACCACCGGCACGCAGACACTCACGAAATGAGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    nicotinic; insect; insecticide; screening; protection agent; conductance; AChR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
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insecticides, or (b) genes which encode polypeptides that are involved i formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
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                                 This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insectiode. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (11). This sequence encodes an acetyl-choline
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                                                                                                                                                                                                                                                                                                                                           0; Mismatches 460; Indels
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Page 19-22; 26pp; German.
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                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1476 AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1536 cceccecarcecarcicaaaccecacececarcicarciacaacacececarcacecearin 1595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1356 CCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACCTTTAATGCAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 AATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACCCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGGGGGGGACGAAGGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1416 ATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTGG
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                                                                                                                                                                                                     New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 512.8; DB 3;
Pred. No. 5.4e-115;
); Mismatches 502;
                             Ë
                             Schulte
                                                                                                                                                                                                                                                                                                        Claim la; Page 8-12; 26pp; German.
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Best Local Similarity 62.5%;
Matches 878; Conservative (
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                             Oellers
                                                                                               2000-014207/02.
                             Adamczewski M,
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                          706 ATAACATTCGCCATTTTGATAAGGCGCAAAACGTTGTACTATTTTTTCAATCTGATTGTG
                                                                                                         766 CCGTGCGTACTGATCGCCTCCATGGCACTGCTAGGGTTTACACTGCCACCAGATTCTGGT
                                                                                                                                      GAAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTG
                                                                                                                                                                   826 GAAAAGCTTCGCTTGGAGTTACAATTCTATTATCGCTTACAGTCTTCCTCAACATGGTG
                ATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                  871 GCGGAGACGATGCCAGCGACGTCGGACGCCGTGCCCTTGCTCGGCACCTA 920
                                                                                                                                                                                                                   GCCGAAACAATGCCGGCGACCTCCGATGCGGTACCGCTGCTCGCTAAGTA
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                                                                                                                                                                                                                                                                                                           ABL07231 standard; cDNA; 1540
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ss.
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P-PSDB; ABB63128.
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Best Local Similarity
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                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elunidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1e-104;
0; Mismatches 225; Indels
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                                                                                          Myers
              23-MAR-2000; 2000US-0191637P
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il Similarity 72.9%;
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P-PSDB; ABB69630.
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4, S 80 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elekaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7377-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly CICGCACTIGGCGGCGCCCGGGGCCTGCTGCTGCTGTGCCTGCTCTGCCTCTCGCCCAGGG Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 U; 0 Other; Claim 1; SEQ ID NO 16175; 21pp + Sequence Listing; English from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Score 458.2; DB 4; Pred. No. 9.6e-102; 0; Mismatches 493;

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CGAGATGCCACCGTGGATCAAGTCCGTTTTCCTACAATGGCTGCCCTGGATCTTGCGAAT 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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                                                                                                                                                                 GCTGGAGCTAAAAGGAGCGCTCCTCCAAATCCCTGGCCCAATGTCCTCGACAA
                                                                                                                                                                                                                       GGAGAATGGCGCGGGGTTGGCGGCGCACAGTTGCTTCGGTGTC---GACTACGAGCTCTC
                                                 GTCACGGCCCGGCTCGGCGACGCCGCCGCCGCCGCGTA---CCTCCGCCGCGGA
                                                                                     GGGTCGACCCGGTCGCAAGATTACACGCAAAACAATACTATTAAGCAATCGCATGAAGGA
                                                                                                                                    CCTGGAGCTGCGCGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCTCGACATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAATTGATCGGCGATTGGAAGTTCGCGCGCAATGGTTGTGGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACATTTCGCGCGACTGGAAGTTCGCCGCCATGGTCGTGGACAG
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                                                                                                            42;
     Length 1509;
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          Score 405.6; DB 4;
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0; Mismatches 604;
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                                                                                                                                                                                                                                                                                           Score 405.6; DB 2; Length 1876;
Pred. No. 7.3e-89;
); Mismatches 604; Indels 42;
                                                                                                                                                                                                         Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor mAChR. nAChR's form ligandgated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal naching acetylcholine receptor, nAChR, alpha 7 subunit. Note: the present sequence decodes to the protein shown in ADA10874 not the one described in the specification
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                                                         Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 0 U; 1 Other;
                                                                                                             27.2%; Score 405.2; DB 6; Length 56.5%; Pred. No. 9.1e-89; ive 1; Mismatches 604; Indels
                                                                                                                                                                      Conservative
                                                                                                                                      Similarity
     encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nicotinic acetylcholine receptor; NAChR; drug screening; NAChR alpha7 subunit; gene; ss.
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neuronal nicotinic acetylcholine receptors, useful for in vitro screening
of a drug substance in a test system specific for humans.
ATTCTGAAGGAGATTA
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR029, PR0341, PR0535, PR0619, PR01030, PR0830, PR0848, PR0943, PR01005, PR01009, PR01021, PR01021, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR02084, PR02145 OR PR02199. PR0 and bused to interact compounds and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocolic disorders, and inflammatory, angiogenic and hybridisation probes used in the isolation of the human PRO sequences.

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0; Mismatches 605;
                                    Gurney AL,
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Pred. No. 1.7e-88;
                                Goddard A,
                                                                                                                                                                                                                                                              PRO polynucleotides encoding
ent, diagnosis and prevention
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                                Baker KP,
Wood WI;
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                                                                              Watanabe CK,
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m 310 Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH. 130 154 214 274 CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA 394 311 ATGGCCAGATTTGGAAACCAGACATTCTTCTTTAAACAGTGCTGATGAGGCGCTTTGACG 370 94 70 The present sequence is the coding sequence for a mutant human alpha7 nicotinic acety/choline gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline 35 CGCCCGCGCGCCTGCTGCTGCTGTGCTCTGCTCTGGCCGAGGGGGGGCACGCTGCGGGT CGCCGGGAGGCGTCTGGCTGGCGCTGGCCGCGTCGCTCCTGCACGTGTCCTGCAAGGCG 95 ACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACAACGTACTGGAGAGGCCCG AGTTCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTGGAGAGAGGCCCG TCGTCAACGAGAGCGACCCGCTGCAGCTCTCCTTCGGCCTCACGCTCATGCAGATCATCG TGGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATCATGG **ACGTGGACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTAAAAACTAGAGTGGAAT**G 191 ACGTGGATGAGAAGAACCAAGTTTTTAACCACCAACATTTGGCTGCAAATGTCTTTGGACAG ATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCAC ATCACTATTTACAGTGGAATGTGTCAGAATATCCAGGGGTGAAGACTGTTCGTTTCCCAG Gaps 42; Sequence 1509 BP; 296 A; 452 C; 429 G; 332 T; 0 U; 0 Other; 605; Indels Score 404; DB 4; Pred. No. 1.7e-88; 0; Mismatches 605 50; Page 69; 77pp; English. 27.2%; Conservative Similarity Matches 839; 251 131 215 155 11 71 275 Query Match 335 Local ò

RESULT 13 AAC90385 ID AAC90385 standard; cDNA; 1509

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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9 AL530299
14 CD013901
11 AK053497
                                                              OM nucleic - nucleic search, using sw model
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achadada	Ephydr	Ephydroidea; Drosophil:	Drosc	idd	idae; Dro		
AUTHORS	Harvey, D.,	',D', B	Brokstei	in, P	., Hong, L., Ev	ans-Holm, M., Su, C.,	Tsang, G.,
TITLE	Lewis, S. and Rubin, G BDGP/HHMI Drosophila	S.and HMI Dr	Rubin osophi	la E	I. ST Project		
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COMMENT	Contact: Sta	t: Staplet	pleton,	ດ≥.	ргиme Г.		
	Lawrence	ice Ber	Berkeley National	Nati			
	Fax: 5	: 510 486 6	796	Date	, ca 3%,	HSO '	
	Email:	http:	*	frui	.fruitfly.org/EST,	est@fruitfly.berkeley.edu	
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/db_xref="taxon:9606"
/clone="CS0DD007YP05"
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    this clone was been removed. hit
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                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/clone="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDRAs were directly ligated into
pOT2. Plasmid cDNA library."
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                                                                                                                                                                                                                                                                                                                        Score 476.2; DB 12; Length 885;
Pred. No. 8.9e-82;
); Mismatches 223; Indels 0;
more T residues at the beginning of the sequence, polyadenylated. The resulting Poly-T sequence has genomic AE003511: arm:X [18722641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
                                                                                                                          organism="Drosophila melanogaster"
                                                                                                                                                                                     'sex="male and female"
                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH16126"
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AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Frac, Web : www.genoscope.cns.fr
BM all: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
ggl-bin/Cluster.cgi?seq=CSODD007CH03QPl&cluster=7646.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/clone_lib="Homo sapiens NEUROBLASTOMA_COT_50-NORMALIZED"
/note="list strand oDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (Dases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Fill-length CDNA libraries and normalization
Unpublished (2001)
On Peb 13, 2001 this sequence version replaced gi:12793792.
                                                          165 GGAACTIATITCAATIGCATTATGTTTATGGTGGCCTCATCAGTTGTGTCAACCATACTT
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Location/Qualifiers
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Pred. No. 1.4e-51;
5; Mismatches 360; Indels
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/organism="Homo sapiens"
//mol type="mRNA"
//db xref="taxon:9606"
/clone_lib="Single gene library"
//note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely vaing M13 forward and reverse primers. Sequencing gaps were closed by re-sequencig using primers flanking the gapped areas."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2296)
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CGGGGTCAAAGATTTAAGAGTGCCACCCCACAGACTATGGAAACCAGACGTCCTTATGTA
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PCR isolation and cloning of novel spli
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Tel: 650 621 8639
Fax: 650 621 8965
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Location/Qualifiers
1. .2296
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                                                                                                                                           Submitted (IG-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Rasagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
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               Sogabe, Y., Tagami, M., Tagawa, A.,
Takeda, Y., Tanaka, T., Tomaru, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE AK053497
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 6enome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapilary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacaba, T. J. Azakawa, K., Akimura, T., Azakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirzaoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itob, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koth, H., Kawai, J., Matsuyama, T., Miyazaki, A., Murata, M., Nakawa, T., Koyawa, T., Koyawa, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1864)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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High-efficiency full-length cDNA cloning Meth. Bnzymol. 303, 19-44 (1999) 9279553 10349636 2 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374	3 Subibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno, H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,R., Skaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Fantonal annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)  The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	dachi, d., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Adachi, d., Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kati, Kawai, J., Kojima, Y., Konda, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matauyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, Y., Salto, R., Salto, R., Salto, R., Salto, R., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Miramahen, M., and Havashi, A., Towaru, A., Toya, T., Yasunishi, A., Miramahen, M., and Havashi, A., Toya, T., Yasunishi, A.,	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (8-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,	υ
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone; A73000/PH4 product: NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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LTVFLLVITETIPSTSELVIPLIGEYLLFTMIFVTLSIVITYSTUNHYRTPTTHRFT
WKAVFLINLLPRVMFWTFYSTEEDBYTRNFYGAELSNLNCFSRADSKSCKEGYPCO
DGTCGYCHHRRVKIGNFSANLTRSSSSESVDAVLSLSALSPEIKEALQSVKYIAENMK
AQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFQPLARARDDT"
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/clone_lib="RIKEN full-length '
/dev_stage="12 days embryo"
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/protein_id="BAC34740.1"
/db_xref="G1:26342156"
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